Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 1.92 Seconds 67.949 Million cell updates/sec Thu May 22 08:50:36 1997; Run on:

Tabular output not generated.

(1-12) from US08653294.pep 98 >US-08-653-294-36 Description: Perfect Score: Title:

1 YRLAIRRIALRY 12 Sednence:

PAM 150 Gap 15 Scoring table:

92623 segs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

a-geneseq26 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part14 9:part9 10:part10 11:part11 12:part12 13:part13 19:part14 15:part15 16:part16 17:part17 18:part18

Mean 19.057; Variance 63.971; scale 0.298 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ž	Result No.	Score	Query Match	Query Match Length	DB	Ω	Description	Pred. No.
•					!			
	-	96	100.0	12	18	R95429	HLA-B2702 84-79-84 pa	2.34e-03
	~	61	62.2	18	13	R71429	Human MHC 1 alpha 1 d	1.74e+01
	m	52	53.1	20	16	R92911	HLA-B2702 CTL modulat	1.27e+02
	4	52	53.1	25	18	R95422	HLAB38.6084.	1.27e+02
	S	25	53.1	25	ထ	R48286	Peptide fragment of H	1.27e+02
	9	52	53.1	25	16	R83093	HLAB38 CTL modulating	1.27e+02
	7	20	51.0		18	R95415	HLA-B7.84-75-84 Palin	1.94e + 02
	<b>ω</b>	20	51.0	20	16	R92913	HLA-B7 CTL modulating	1.94e + 02
	σ	49	50.0		18	R95425	HLA-B2702.75-84(D).	2.40e+02
	10	49	50.0		18	R95413	Alphal-helix of HLA-B	2.40e+02
	11	49	50.0		œ	R41208	Peptide fragment of C	2.40e+02
	12	49	50.0		18	R95430	HLA-B2702 84-75T/75-8	2.40e+02
	13	49	50.0	20	78	R95428	HLA-B2702 84-75-84 pa	2.40e+02
	14	49	50.0		٦	R05012	Papilloma virus type	2.40e+02
	15	49	50.0	25	18	R95416		2.40e+02
	16	49	50.0		ω	R41205	Peptide fragment of C	2.40e+02
	17	49	50.0	25	16	R83090	HLA-B2702 CTL modulat	2.40e+02

Note: Post-processor removed 28 summaries from list due to search parameters chosen.

# ALIGNMENTS

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Fight 1, 1954.1 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the characteristic party of the protein protein associated antigens. This sequences can be used to isolate the protein protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. This found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HiA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with LA-B2702.604 (see F89416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (Apcs), by adding to the mix the extracellular portion of $74, in an amount sufficient to compete containing the binding of the p74 ligand.
                                                                                                                                                                                HIA-B2702 84-79-84 palindrome.
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example: Page 12; 29pp; English. Resemble: Page 18:5415-R95411 represent palindromes and fragments of R95413; and R95413-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 2.34e-03;
0; Mismatches 0; Indels
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10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                cytolysis; antigen presenting cell
                                                    standard; peptide; 12 AA.
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Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krensky AM;
                                                                                                                                          12-NOV-1996 (first entry)
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                                           R95429
SUPPLIES OF SUPPLI
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1 YRLAIRRIALRY 12

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.T. 2 R71429 standard; peptide; 18 AA. 12429; (first entry)

Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).

Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.

W09505189-A. RESULT TO DIT RESULT RE

WO95050.2.
23-FE91995.
12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.

Goldstein A, Goodenow RS, Olsson L; WPI; 95-088577/13. Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface

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Compsns. comprising lymphoid surface membrane proteins - which may inhibit eytolytic activity and differentiation of CTLs. Example: Page 9: 29pp: English. R95413, and R95415-R95431 represent palindromes and fragments of
                            10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-1994 (first entry)
Peptide fragment of HLA-B38 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R48286 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%;
larity 66.7%;
Conservative
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larity 66.7%;
Conservative
                                                                                               Krensky AM;
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Matches 8; Conser
                                                                                        Clayberger C, Kr
WPI; 95-194027/25
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Best Local S
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R83061-R83085, R83090-R831996 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a diner of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; rcell lysate; membrane protein; mammal; heat shock protein; Esc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation; cytolysis; antigen presenting cell.
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
                      Example 4; Page 45; 103pp; English.
R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
receptors. Via competitive inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
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                                                                                                                                                                                                                                                                                                      Score 61; DB 13; Length 18;
Pred. No. 1.74e+01;
4; Mismatches 2; Indels
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Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R95422;
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llarity 66.7%;
Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity
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WPI; 95-358582/46.
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                                                                                                                                                                                                                                             18 AA;
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receptor
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Numerical lyasts. Associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HLAB38.6084. These sequences can be used to isolate the protein p74 from a T-cell lyaste. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B7702 palindromic peptide.

Compositions comprising the extracellular fragment of P74 combined with CHLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic I lymphocyte (CLL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of CT-cells, by combining them with the extracellular portion of P74 and determining the amount of binding between the candidate compound and p74.

Containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing the binding of the P74 ligand.
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26-FEB-1993; U01758.

27 25-FEB-1993; U01758.

28 GSTRD ) UNIV LELAND STANFORD JUNIOR.

29 GSTRD ) UNIV LELAND STANFORD JUNIOR.

20 Clayberger CA, Krensky AM;

20 STANS STANS STANFORD THA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets

27 Example 13; Page 39; 61pp; English.

28 Example 13; Page 39; 61pp; English.

29 Example 13; Page 39; 61pp; English.

20 This peptide is used to modulate cytocoxic T-lymphocyte (CTL)

20 Cativity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL

20 Cativity in parasaltic diseases and neoplasia and in studies on viral

21 Infection. The peptide can also be used for identifying CTLs which

22 Chis peptide is derived from the HLA-B38 antigen and corresponds

23 Chis peptide is derived from the HLA-B38 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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represent palindromes and
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Pred. No. 1.27e+02;
1; Mismatches 2;
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18-MAY-1995

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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Example 13; Page 32; 80pp; English.
R83061-R83065 and R92207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R95415 standard; peptide; 20 AA.
R95415,
12-NOV-1996 (first entry)
HLA-B7.84-75-84 Palindrome.
HLA: P7.4; alphal helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                HLAB38 CTL modulating peftide (B38.5084).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human-leucocyte-associated antigens. This sequence represents the Hila-B7.84 painforme. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CILs. Example; Page 18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                    12-OCT-1995.
05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytolysis; antigen presenting cell.
                                                                         R83093 standard; peptide; 25 AA
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similarity 66.7%;
8; Conservative
                                                                                                              16-MAY-1996 (first entry)
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1 YRLAIRRIALRY 12
                                                                                                                                                                                           class I MHC; HLAB38
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Best Local Similarity
Matches 8; Conser
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WPI; 95-358582/46.
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W09513288-A1.
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WO9526979-Al.
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompeatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B7. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds the amount of binding between the candidate compound determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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05-APR-1994; US-222851.
05-APR-1994; US-222851.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using class I B75-84 MHC antigen of the recipient
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Pred. No. 1.94e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 18;
Pred. No. 1.94e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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R92913 standard; peptide; 20 AA.
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Clayberger CA, Krensky AM; WPI; 93-303134/38.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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ID R9

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                                                                                                                                                                                                                                                                                                                                 Companie, regarding lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 11: 29pp: English.

CS 55413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the R5413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the protein pv4 from a T-cell lysate. P74 is a T-cell surface membrane protein pv4 from a T-cell lysate. P74 is a T-cell surface membrane protein cassociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on a mphoteric detergent, and then passed through an affinity column compatibing a covalently bound HAA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HA-B2702.60-84 (see R95416), indices calcum influx, and inhibits compositions can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the p74 ligand.

CALL APA STATE APA for the binding of the p74 ligand.
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This sequence represents the alphal-helix of the human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, particularly palidher antigen B2702 (HLA-B2702). This sequence, protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 2.40e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                   10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                Location/Qualifiers
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R95413 standard; peptide; 10
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Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                             Krensky AM;
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                                                                                             "N3D mutation"
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WPI; 95-194027/25.
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                                                         Misc_difference 3
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WO9513288-A1.
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Synthetic.
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cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of P74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds the amount of binding between the candidate compound the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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R95430.
12-NOV-1996 (first entry)
12-NOV-1996 (first palindrome.
HIA-B2702 84-75£7/75-84T palindrome.
B cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; cytolysis; antigen presenting cell.
Synthetic.
Synthetic.
Synthetic.
18-MAY-1995.
10-NOV-1994; U12985.
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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
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R41208;
115-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
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Pred. No. 2.40e+02;
"...matrhes 0; Indels
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Pred. No. 2.40e+02;
0; Mismatches 0; Indels
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25-FBE-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
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WPI; 95-194027/25
                                                                                                   20 AA;
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W09513288-A1.
                                                                                                                                                                                                                               1 yrlair 6
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| YRLAIR
                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                          Sequence
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  8888888
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                                                                     WILL'S JS-1940/12/25.

WHILL'S JS-1940/12/25.

WHILL'S JS-1940/12/25.

WHILL'S JS-1940/12/25.

Example: Page 12: 29pp: English.

Example: Page 12: 20pp: 20pp: English.

Example: Page 12: 20pp: English.

Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tompsis. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: Bng11sh.

Example: Page 13: 20pp: Bng11sh.

Manan-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a manalian T-cells, and is also immunologically cross reactive with the heat shock protein H8c70.

The protein associated with T-cell activation in manmalian T-cells, and is a surface and in a limited number of cell types, but is particularly compared in a limited number of cell types, but is particularly collumn containing a covalently bound HA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis.
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HLA-B3702 84-75-84 palindrome.
HLA-B3702 84-75-84 palindrome.
HLA-B3702 84-75-84 palindrome.
The D74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytofoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
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10-NOV-1993; US-150493.
(STRD) UNIV LELAND STANFORD JUNIOR.
CLAYDERGER C, KIENSKY AM;
WPI; 95-194027/25.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR
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R95428 standard; peptide; 20 AA.
R95428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                       Clayberger C, Krensky AM; WPI; 95-194027/25.
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WO9513288-A1.
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Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Stanple, Page 9; 29pp. English. Raspels; 29pp. English. R85413, and R95415-R85431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents HLA-B2702.60-84. These sequences can be used to isolate the protein.p34.
determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-1990 (first entry)
Papilloma virus type 16 L2 peptide no. 55.
Papilloma virus; PV type 16; immunoglobulin; L2; ELISA: cervical cancer.
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Dillner J, Dillner L;

WPI: 90-164122/21.

Detecting papillona virus infections - by identifying specific antibodies against partic. viral proteins or fragments, esp. for rapid diagnosis of cervical cancer.

Disclosure; 7pp; English.

The peptide is one of 66 overlapping peptides which together cover the entire sequences of the Li and L2 proteins of human PV type 16. The peptide was found to be unreactive with Ig Abs in the sera of petients with type 16 cervical cancer.

See also R04958-R05023.
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Pred. No. 2.40e+02;
3; Mismatches 2; Indels
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10-NOY-1994; U12985.
10-NOY-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R05012 standard; protein; 20 AA.
R05012;
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llarity 50.0%;
Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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30-OCT-1989; SE0612.
28-OCT-1989; SE-003870.
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crown a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Has70. p74 is found in a limited number of cell types, but is particularly expressed on and T cells. p74 can be isolated by lysis of a suitable cell with an affinity column containing a covalently bound HLA-122702 palindromic peptide.

CC ompositions comprising the extracellular fragment of p74 combined with cclums containing a covalently bound HLA-122702 palindromic peptide.

CC ompositions comprising the extracellular fragment of p74 combined with be sequence, induces calcium influx, and inhibits expectors.

CC pymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing cc extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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Query Match 50.0%; Score 49; DB 18; Length 25; Best Local Similarity 100.0%; Pred. No. 2.40e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

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Search completed: Thu May 22 08:50:42 1997 Job time : 6 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:36:18 1997; MasPar time 2.92 Seconds 116.962 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-36 (1-12) from US08653294.pep 98

1 YRLAIRRIALRY 12 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir50 Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 26.905; Variance 45.950; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Gaps

; 0

Score 63; DB 11; Length 128; Pred. No. 2.74e+00; 4; Mismatches 1; Indels

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

113 yilsvrrltlr 123 | |::||::|| | YRLAIRRIALR 11

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Result No. So	Score	Query	Query Match Length	DB	ΙD	Description	Pred. No.
	63	64.3	128	11	S69745	hypothetical protein	2.74e+00
C	28	59.2	388	16	S15593	hypothetical protein	1.59e+01
m	57	58.2		2	S17776		2.23e+01
-	22	58.3		9	229990	histocompatibility a	2.23e+01
10	26	57.1	78	10	F64429	DNA-directed RNA pol	3.13e+01
w	26	57.1	416	m	ACCH3N	nicotinic acetylchol	3.13e+01
7	26	57.1		16	S60589	acetylcholine recept	3.13e+01
æ	26	57.1		7	A24572	nicotinic acetylchol	3.13e+01
o.	26	57.1	503	7	A53956	nicotinic acetylchol	3.13e+01
_	26	57.1		12	B48327	COI intron alpha-sen	3.13e+01
_	26	57.1		H	A41529	GRR1 protein - yeast	3.13e+01
~	52	56.1		14	148752		4.36e+01
~	22	56.1	212	11	S17476		4.36e+01
=+	22	56.1		2	S44230		4.36e+01
ហ	55	56.1		ო	ACBOE	nicotinic acetylchol	4.36e+01
16	22	56.1		7	S34775	nicotinic acetylchol	4.36e+01
7	55	56.1	511	ដ	S38905	hypothetical protein	4.36e+01
m	55	56.1		ω	538642	chaperonin-60 alpha	4.36e+01
Φ.	55	56.1		ហ	A32869	apolipoprotein(a) (E	4.36e+01
0	22	56.1	2242	12	A57541	pyrimidine synthesis	4.36e+01
_,	54	55.1	267	16	S44225	strf protein - Strep	6.05e+01

SENCE S15591
Fauthors S15591
# authors Pfeifer, F.; Blaseio, U.
# fournal Nucleic Acids Res. (1990) 18:6921-6925
# fittle Transposition burst of the ISH27 insertion element family in Harbos-references MUID:91088266
# accession S15593

ACCESSIONS REFERENCE

ORGANISM

DATE

RESULT ENTRY TITLE

S15593 #type complete
hypothetical protein (insertion sequence ISH27-3) Halobacterium halobium
#formal\_name Halobacterium halobium
21-Nov-1993 #sequence\_revision 21-Nov-1993 #text\_change

	Yeas of the poly o	#type complete   protein YDR360w - yeast (Saccharomyces   saccharomyces cerevisiae   sequence_revision 06-Sep-1996 #text_change	the EMBL Data Library, June 1995 of S. cerevisiae cosmid 9476. label DUZ U28372 #molecular-weight 14014 #checksum 3949
S44228 S53849 S55114 ACMSE ACRTE S12899 S47750 WQBSGS	333926 S04717 J0555 S04717 1481120 1481120 1481120 1481120 1481123 ACCH4N A44214 GNWV16	ALIGNMENTS S69745 #type complete hypothetical protein YDR360w cerevisiae) #formal_name Saccharomyces cc 23-Aug-1996 #sequence_revisic 66-Sep-1996	d to the EMEL. ence of S. cer. 28 ##label DUZ EMBL:UZ8372
01110	4 111111 H H H H H H H H H H H H H H H H	# ty] P P P P P P P P P P P P P P P P P P P	o the of ##1a]
7 4 4 4 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1 1 8 8 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	\$69745 #ty hypothetical cerevisiae) #formal_name \$ 23.Aug.1996 #s 06-5ep-1996 \$69745	0) 51 42 11
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00000000000000000000000000000000000000	J M W M M M M M M M M M M M M M M M M M	RESULT ENTRY TITLE ORGANISM DATE ACCESSIONS	REFERENCE #authors #submission #description #accession #arcessidues ##residues ##residues ##residues ##residues ##residues ##residues ##residues ##residues

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F64429 #type complete

DNA-directed RNA polymerase (EC 2.7.7.6) subunit H -

Methanococcus jannaschii

13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
13-Sep-1996
F64430

Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton,
R.A.; Gocayne, J.D.; Rerlavage, A.R.; Dougherty, B.A.;
Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeer, R.;
Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
J.L.; Nouyen, D.; Ulterback, T.R.; Kelley, J.M.; Glodek,
J.L.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Rlenk,
H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
Science (1996) 273:L058-1073
COmplete genome sequence of the methanogenic archaeon,
F64429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M. #journal EMBO J. (1988) 7:595-601 Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nicotinic acetylcholine receptor alpha-3 chain, neuronal chicken (fragment)
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30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; nucleic acid sequence not shown;
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#length 78 #molecular-weight 9001 #checksum 3754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-78 ##label BUL
##cross-references GB:L77117; TIGR:MJ1039; CDS_PID:91511063
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Pred. No. 3.13e+01;
1; Mismatches 1; Indels
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##molecule_type DNA; mRNA
##residues 1-416 ##label NEF
##cross-references EMBL:X07345
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#start_codon TTG
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S00378; A38755
S00376
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184-202
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mansouri, K.; Piepersberg, W.
Mol. Gen. Genet. (1991) 228:459-469
Genetics of streptomycin production in Streptomyces griseus:
nucleotide sequence of five genes, strFGHIK, including a
phosphatase gene.
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strr protein - Streptomyces griseus
#formal_name Streptomyces griseus
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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##residues 1-388 ##label PFE
##cross-references EMBL:X54434
XX #length 388 #molecular-weight 44571 #checksum 1952
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submitted to the EMBL Data Library, February 1993
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FICATION #superfamily class I histocompatibility antigen;
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Pred. No. 2.23e+01;
2; Mismatches 1; Indels
                                                                                     Length 388;
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Pred. No. 2.23e+01;
4; Mismatches 1; Indels
                                                                                   Score 58; DB 16; Le
Pred. No. 1.59e+01;
2; Mismatches 0;
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##residues 1-281 ##label MAN
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##residues
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Similarity 70.0%;
7; Conservative
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#label MAT
#length 499 #molecular-weight 57347 #checksum 1936
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#disulfide_bonds #status predicted\
#binding_site carbohydrate (Asn) (covalent) #status
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acetylcholine receptor alpha chain precursor - bovine
#formal_name Bos primiqenius taurus #common_name cattle
27-Apr-1996 #sequence_revision 27-Apr-1996 #text_change
S60589
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#journal Nature (1986) 319:368-374

#title Isolation of a CDNA clone coding for a possible neural nicotinic actylcholine receptor alpha-subunit.

#cross-references MUID:86118671

#accession A24572
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30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
15-Jun-1996
A24572
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Neurochem. Res. (1992) 17:281-287
Primary structure of an agonist binding subunit of the
nicotinic acetylcholine receptor from bovine adrenal
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Pred. No. 3.13e+01;
2; Mismatches 3; Indels
                                                                                  Score 56; DB 3; Length 416; Pred. No. 3.13e+01; 2; Mismatches 3; Indels
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#length 416 #checksum 3404
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Y #length 495 #molecu
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Cummings, D.J.; Michel, F.; McNally, K.L.
Curr. Genet. (1989) 16:381-406
DNA sequence analysis of the 4.5 kilobase pair cytochrome oxidase subunit I mitochondrial gene from Podospora
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Exp. Neurol. (1991) 111:175-180
Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal acetylcholine receptor.
                                                                                                    A53956 #type complete
nicotinic acetylcholine receptor alpha-3 chain precursor,
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COI intron alpha-sen DNA protein - Podospora anserina
mitcochondrion (5GC3)
#formal name mitcochondrion Podospora anserina
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                            neuronal - human
#formal_name Homo sapiens #common_name man
07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change
06-Sep-1996
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#length 788 #molecular-weight 89463 #checksum 3000
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#submission submitted to the EMBL Data Library, June 1990
#description Nucleotide sequence of the mature human nicotinic
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##cross-references GDB:125219
#map_position 15q24-15q24
CLASSIFICATION #superfamily acetylcholine receptor
SUMMARY #length 503 #molecular-weight 57153 #checksum
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Pred. No. 3.13e+01;
2; Mismatches 3; Indels
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##cross-references GB:X55026; GB:M30937; GB:M61734
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#molecule_type mRNA
##racidues 30.503 ##label ANA
##cross-references EMBL:X53559
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##cross-references GB:M37981
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Similarity 58.3%;
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gene name RXRbetal
#length 176 #checksum 8478
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##residues 1-212 ##label RAM
##cross-references EMBL:X59720
NNCE S19350
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|larity 77.8%; |
|Conservative
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                                                                                                                                                                      56.1%;
llarity 66.7%;
Conservative
                                ##molecule_type_DNA
##residues 1-17
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##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                       #authors Flick, J.S.; Johnston, M.
#journal Mol. Cell. Biol. (1991) 11:5101-5112
#title GRR1 of Saccharomyces cerevisiae is required for glucose
#title repression and encodes a protein with leucine-rich repeats.
#cross-references MUID:92017785
#accession A41529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Nagate, T.; Kanno, Y.; Ozato, K.; Taketo, M.
#journal Gene (1994) 142:183-189
#title The mouse Rxrb gene encoding RXR beta: genomic organization and two mRNA isoforms generated by alternative splicing of transcripts initiated from CpG island promoters.
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submitted to the Protein Sequence Database, September 1995
857109
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submitted to the Protein Sequence Database, September 1995
857111
                                                   Gaps
                                                                                                                                                                                  A41529 #type complete
GRR1 protein - yeast (Saccharomyces cerevisiae)
protein J1885; protein Y370900c.
#formal_name_Saccharomyces cerevisiae
30.Jun-1992_#sequence_revision 30.Jun-1992 #text_change
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gene RxRbetal protein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
02-7ul-1996 #sequence_revision 02-7ul-1996 #text_change
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#length 1151 #molecular-weight 132733 #checksum 1173
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Pred. No. 3.13e+01;
4; Mismatches 3; Indels
          Score 56; DB 12; Length 788;
Pred. No. 3.13e+01;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     13-Sep-1995
A41529; S57109; S57111; S17487
                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-1151 ##label FLI
##cross-references GB:M59247
SNCE S57085
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##residues
##cross-references EMBL:249590
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##residues 1-2 ##label RAM
##cross-references EMBL:249590
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Best Local Similarity 41.7%;
Matches 5; Conservative
        Best Local Similarity 70.0%;
Matches 7: Concounty 70.0%;
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KEYWORDS tand
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Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, K.; Ramezani
Rad, M.; Xu, G.
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East (1991) 7:533-538
The complete sequence of a 11,953 bp fragment from ClG on chromosome III encompasses four new open reading frames.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical, protein YCL186
#formal_name Saccharomyces cerevisiae
12.mar-1993 #sequence_revision 12.mar-1993 #text_change
24.Feb-1995 $
$17476; $19362
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#formal_name Streptomyces glaucescens
13-3an-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
844230
844224
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                                                                                                                                                                                                                                                                                                                                                                                                                                 S17476 #type complete
hypothetical protein YCL034w - yeast (Saccharomyces
cerevisiae)
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SUMMARY #length 212 #molecular-weight 23590 #checksum 526
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###CSIGNES T-176 ##label RES ##cross-references EMBL:X72017; NID:g510152; CDS_PID:g510153
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                                                                                                                                                                                    Length 176;
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Pred. No. 4.36e+01;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                   0; Indels
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Pred. No. 4.36e+01;
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RESULT ENTRY

셤

DATE

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#domain signal sequence #status predicted #label SIG\
#product acetylcholine receptor epsilon chain #status
predicted #label MAT\
#domain transmembrane #status predicted #label TMI\
#binding_site carbohydrate (Asn) (covalent) #status
predicted*
#lainding_site carbohydrate (Asn) (covalent) #status
predicted\
#disulfide_bonds #status predicted
#length 491 #molecular-weight 54565 #checksum 7419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-491 ##label TAK

"The epsilon chain can replace the gamma chain to form a functional receptor molecule.

FICATION #superfamily acetylcholine receptor glycoprotein; fon channel; neurotransmitter receptor, postsynaptic membrane; transmembrane protein
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Takai, T.; Noda, M.; Mishina, M.; Shimizu, S.; Furutani, Y.; Kayano, T.; Ikeda, T.; Kubo, T.; Takahashi, H.; Takahashi, H.; Takahashi, H.; Takahashi, H.; Takahashi, M.; Numa, S.
T.; Kuno, M.; Numa, S.
#journal Nature (1985) 315:761-764

#title Cloning, sequencing and expression of cDNA for a novel subunit of acetylcholine receptor from calf muscle.
#cross-references MUID:85240565
                                                                                                                                                                                                                                                                                                                                                                                                 ACBOE #type complete nicotinic acetylcholine receptor epsilon chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Bos primigenius taurus #common_name cattle 28-reb-1986 #sequence_revision 28-Feb-1986 #text_change 08-Dec-1994
                                                                                                                                                                                                   Gaps
                                                                     #start_codon GTG
SUMMARY #length 281 #molecular-weight 31427 #checksum 4100
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Pred. No. 4.36e+01;
1; Mismatches 4; Indels
                                                                                                                                             Score 55; DB 10; Length 281
Pred. No. 4.36e+01;
2; Mismatches 1; Indels
##residues 1-281 ##label MAY
##cross-references EMBL:X78974
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
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##molecule_type mRNA
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Search completed: Thu May 22 08:36:46 1997 Job time: 28 secs.

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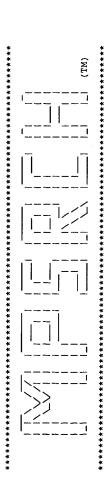
Gaps

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232 ysliirrkplfy 243 

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu May 22 08:34:07 1997; MasPar time 2.32 Seconds 182.533 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-31 (1-20) from US08653294.pep 154 1 YRLAIRLNERYRLAIRLNER 20 Title: Description: Perfect Score:

Scoring table: Sequence:

PAM 150 Gap 15

59021 seqs, 21210388 residues

Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 30.299; Variance 54.375; scale 0.557 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	9.83e-01	1.38e+00	1.38e+00	2.71e+00	2.71e+00	2.71e+00	2.71e+00	2.71e+00	3.77e+00	3.77e+00	7.24e+00	7.24e+00	9.99e+00	9.99e+00	9.99e+00	1.37e+01	1.37e+01	1.37e+01	1.37e+01	1.37e+01	1.88e + 01	1.88e+01
Description	5-EXO-ALCOHOL DEHYDRO	TYPE 4 PREPILIN-LIKE	DNA POLYMERASE II (EC	PHYCOBILISOME ROD-COR	PHYCOBILISOME ROD-COR	NITROGEN REGULATION P	INTEGRIN ALPHA-3 PREC	INTEGRIN ALPHA-3 PREC	ADP-HEPTOSELPS HEPT	HYPOTHETICAL 48.0 KD	NITROGEN REGULATION P	72 KD CRYSTAL PROTEIN	BETA-GLUCURONIDASE PR	NITRITE REDUCTASE (NA	NUCLEAR PORE COMPLEX	HYPOTHETICAL GENE 52	GLYCOPROTEIN C PRECUR	GLYPICAN-3 PRECURSOR	GLYPICAN-3 PRECURSOR	ALPHA-AMYLASE (EC 3.2	PROTEIN KINASE PKNA.	60S RIBOSOMAL PROTEIN
a	FDEH_PSEPU	LEP3_ERWCA	DPO2_ECOLI	PYG4_ANASP	PYG3_MASLA	NTRB_ECOLI	ITA3_CRISP	ITA3_HUMAN	RFAF_HAEIN	YOO5_CAEEL	NTRB_SALTY	CR72_BACTI	BGLR_RAT	NIR_EMENI	N358_HUMAN	VG52_HSVSA	VGLC_HSVE4	GPC3_HUMAN	GPC3_RAT	AMY_PYRFU	PKNA_MYCLE	RL5_SCHPO
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% Query Match Length DB	361	279	782	252	253	349	1051	1051	346	424	349	643	648	1104	3224	115	485	580	597	648	253	293
Query Match	46.1	45.5	45.5	44.2	44.2	44.2	44.2	44.2	43.5	43.5	42.2	42.2	41.6	41.6	41.6	40.9	40.9	40.9	40.9	40.9	40.3	40.3
Score	71	70	70	68	68	89	68	68	67	67	65	65	64	64	64	63	63	63	63	63	62	62
Result No.	-	7	3	4	5	ø	7	∞	თ	10	11	12	13	14	15	16	17	18	19	20	21	22

DB 3; Length 361;

46.1%; Score 71;

Query Match

1.88e+01 1.88e+01 1.88e+01 2.57e+01 2.57e+01 2.57e+01 2.57e+01 2.57e+01 2.57e+01 2.57e+01 3.49e+01 3.49e+01 3.49e+01 3.49e+01 3.49e+01 3.49e+01	1000
PROTEIN S10. SIT4-ASSCCIATING PROT NITRITE REDUCTASE (NA 3'-PHOSPHOADENOSINE 5 GALACTOSIDE 2-L-PUCOS HYPOTHETICAL 39.3 KD HYPOTHETICAL 39.3 KD HYPOTHETICAL 39.3 KD HYPOTHETICAL 39.3 KD PROTEIN GLUTAMINE GAM PROTEIN GLUTAMINE GAM PROTEIN GLUTAMINE GAM PROTEIN GLUTAMINE GAM AVIRULENCE A PROTEIN. RETINOBLASTOMA ASSOCI CYPI ACTIVATORY PROTE DELTA-(L-ALPHA-AMINOA PROTEIN UG8. TRNA PSEUDOURIDINE 55 DIHYDROFIAVONOL-4-RED HYPOTHETICAL 40.5 KD CELLULAR TUMOR ANTIGE KUP SYSTEM POTASSIUM AMP-DERENDENT DNA HEL	TOO WILLIAM BOOK TOWN
VP10_RBSDV SAP4_YERST WIR_NEDCR CYSH_THIRO FUT2_RABIT YV29_MYCTU PH84_YEAST TPOR_HUMAN TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE TGLC_MOUSE T	70000
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558 11176 1176 1239 358 358 685 685 927 114 3712 312 337 337 337 337 337 337 337 337 337	1 3
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### ALIGNMENTS

AA.	(3.	(FDEH).		SCOTOBACTERIA; AEROBIC RODS AND COCCI;		.00.		HORITACH .			OF 1-45.			TAKEUCHI K., HORIUCHI T.,			"HOR + NAD(+) =		DEHYDROGENASE.	OF CAMPHOR.		ZINC-CONTAINING ALCOHOL DEHYDROGENASE								(BY	(BY SI	ATOM) (BY	(BY	E)	TIC) (BY SIMILARITY).	:RC32;
361	UPDAT	ON UPD .1)		ERIA;		TO 97-100.		M TOSOH	993).		SEQUENCE			TAKEUC			XYCAMP					-CONTA								CATALYTIC)	CATALYTIC)	SECOND	SECOND	SECOND	CATALYTIC)	E46D28F7 CRC32
PRT;	ED) SEQUENCE UPDATE)	ANNOTATION UPDATE E (EC 1.1.1) (FD)		COTOBACT		AND REVISIONS T		A HOS	ACTA 1174:91-94(1993)	•	AND			ы Э		(1986).	5-EXO-HYDROXYCAMPHOR	ЭН.	ZINC-CONTAINING	PATHWAY: SECOND STEP FOR CATABOLISM		THE			SEO.					ZINC	ZINC	ZINC	ZINC	_	Z I	MW; E46D
STANDARD;	CREA	34, LAST DROGENASE		CUIES; S				מאקאטאט	CTA 1174		1-100 FROM N.A.,			, YAMAGUCHI		089-1095	TIX: 5-E	IOR + NADH.	IS A ZIN	STEP FC	AMPHOR.	SIMILARITY: BELONGS TO		ï	5; ALT			DH_ZINC.	C; NAD.	40	62	85	101	104	170	38460 N
STAN		(REL. 3 OL DEHYD		GRACILICUTES;	ACEAE.	OM N.A.,	17453;	93326643. H KOGA H					86223770.	ARAMAKI H.,	I.C.;	L. 166:1	IC ACTIVITY:	2,5-DIKETOCAMPHOR +	COFACTOR: THIS IS A	: SECOND	INDUCTION: BY CAMPHOR	ITY: BEL			••	A29844	7; IADF.	9	ASE; ZINC;	40	62	80	101	104		361 AA;
FDEH_PSEPU	01-MAR-1989 01-OCT-1996	01-OCT-1996 (REL. 34, LAST ANNOTATION UPC 5-EXO-ALCOHOL DEHYDROGENASE (EC 1.1.1)	PSEUDOMONAS	PROKARYOTA;	F3EUDOMONADACEAE	SEQUENCE FROM N.A.,		ARBULINE; 93.	•	[2]	SEQUENCE OF	H				J. BACTERIOL. 166:1089-1095(1986)	-!- CATALYTIC	2,5-DIK	- ( - COFACTO)	-!- PATHWAY		-!- SIMILAR					$\circ$	PROSITE; PS(	OXIDOREDUCTASE;	METAL	METAL	METAL	METAL	METAL		SEQUENCE
RESULT ID F	A P P	S E E	So	88	2 2 2	장	S :	X X	Z.	RN	RP	ည္ထ	RX	RA	RA	RL	႘	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	DR	DR	DR.	DR	DR	ΚM	H	FI	ЕJ	E I	E I	H (	S

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MEDLINE; 91017565.

BONNER C.A., HAYS S., MCENTEE K., GOODWAN M.F.;

PROC. NATL. ACAD. SCI. U.S.A. 87:7663-7667(1990).

-! FUNCTION: THOUGH TO BE INVOLVED IN DNA REPAIR AND/OR MUTAGENESIS.

-! CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE —
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G -> A (IN REF. 2).
EH -> DD (IN REF. 4).
R -> G (IN REF. 4).
N -> T (IN REF. 2).
LDYQRSPLDYEHYLTRQLQPYAEGILPFIEDNEATL
MTGQLGLF. -> PGLPTFTTGLTRTLSDPPATTRGG
NTPFY (IN REF. 2).
WP. 0762928E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOGENE; EG10747; POLB.
PROSITE; PS00116; DNA_POLYMERASE_B.
DNA-DIRECTED DNA POLYMERASE; SOS RESPONSE; DNA REPAIR; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                   N PYROPHOSPHATE + DNA(N).
-!- ENZYME REGULATION: DNA POLYMERASE II ACTIVITY IS REGULATED
THE LEXA GENE DIRING THE SOS RESPONSE.
-!- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
MEDLINE; 92077441.
BRYANT D.A., STIREWALT V.L., GLAUSER M., FRANK G., SIDLER W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-010-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNORATION UPDATE)
PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG4 (L-RC 29.2).
                                                                                                                                                                                      MEDLINE, 92334977.
MEDLINE, 92334977.
YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA
ISONO K., MIZOBUCHI K., NAKATA A.;
NUCLEIC ACIDS RES. 20:3309-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 3; Length 782;
Pred. No. 1.38e+00;
4; Mismatches 4; Indels
                                                                   STRAIN-K12;
MEDLINE; 91083835.
CHEN H., SUN Y., STARK T., BEATTIE W., MOSES R.E.;
DNA CELL BIOL. 9:631-635(1990).
                                                                                                                                                                                                                                                                 [4]
SEQUENCE OF 1-457 FROM N.A., AND SEQUENCE OF 1-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANABAENA SP. (STRAIN PCC 7120).
PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                   40L. GEN. GENET. 226:24-33(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X54847; G581193; -.
EMBL; M37727; G145746; -.
EMBL; M62646; G147318; -.
EMBL; M35371; E27155; ALT_SEQ.
EMBL; M38283; G705349; -.
EMBL; D10483; G288766; -.
PIR; S15943; JDEC22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         782 AA; 89921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.5%;
Similarity 50.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 rmlqkhaeryrlplrl 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLAIRLNERYRLAIRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B36236; B36236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                [2]
SEQUENCE FROM N.A.
                                                                                                                                           [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYG4_ANASP
P29989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
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                     g
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WALKER S., SALMOND G.P.C.;
MOL. MICROBIOL. 8:443-456(1993).
MOL. MICROBIOL. 8:443-456(1993).
MICROBIOL. B:443-456(1993).
MOL. MICROBIOL. B:443-456(1993).
MOL. MICROBIOL. B:443-456(1993).
MOL. MICROBIOL. B:443-456(1993).
MICROBIOL. B:443-456(1993).
MICROBIOL. B:443-456(1993).
MICROBIOL. B:443-456(1993).
MICROBIOL. B:443-456(1993).
MICROBIOL. MICROBIOL. MICROBIOL. B:443-456(1993).
MICROBIOL. MICROBIOL. MICROBIOL. MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                          01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
TYPE 4 PREPILIN-LIKE PROTEIN SPECIFIC LEADER PEPTIDASE (EC 3.4.99.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROBABLE).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C20; ALSO KNOWN AS TYPE III LEADER PEPTIDASE FAMILY.
EMBL; X70049; G581154; -.
PIR; S31758; S31758.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                              PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC ENTEROBACTERIACEAE.
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SCRII93;
MEDLINE; 93316842.
REEVES P.J., WHITCOMBE D., WHARAM S., GIBSON M., ALLISON G., BUNCE N., BARALLON R., DOUGLAS P., MULHOLLAND V., STEVENS S., WALKER S., SALMOND G.P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASE; PROTEASE; TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.
TRANSMEM 10 30 POTENTIAL.
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
STRAIN=K12 / W3110;
MEDLINE; 91238699.
IWASAKI H., ISHINO Y., TOH H., NAKATA A., SHINAGAWA H.;
. 9.83e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
7, 02B5DC02 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 5; L
Pred. No. 1.38e+00;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
POLB OR DINA.
                                    Mismatches
                                                                                                                                                                            279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      782 AA
                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31131 MW;
                                                                    316 qlaarlqdrypladlitgr 334
                                                                                                   2 RLAIRLNERYRLAIRLNER 20
                Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 yrlpimlerrwrqdiele 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
257
279 AA;
                                                                                                                                                                                                                                                                                                              ERWINIA CAROTOVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                        LT 2
LEP3_ERWCA
P31712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 3
DPO2_ECOLI
P21189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
TRANSMEM
SEQUENCE
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TRANSMEM
TRANSMEM
TRANSMEM
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Gaps

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252 AA

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ZUBER H.

THE CORE

INIT\_MET SEQUENCE

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NINFA A.J., BENNETT R.L.;
J. BIOL. CHEM. 266:6888-6893(1991).
-!- FUNCTION: WIRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF WIRC. IN NITROGEN LIMITATION WIRB ACTIVATES NINC BY PHOSPHORYLATING IT, WHILE IN NITROGEN EXCESS NIRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
                                                                                                                                                    PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INACTIVATED BY NTRB.
                                                                                                                                                                                                                                                                 MIRANDA-RIOS J., SANCHEZ-PESCADOR R., URDEA M., COVARRUBIAS A.A.;
NUCLEIC ACIDS RES. 15:2757-2770(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-).
THE (BY SIMILARITY).
5 GR017919 CRC32;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 9334796.
PLUNKETT G. III, BURLAND V.D., DANIELS D.L., BLATTNER F.R.;
NUCLEIC ACIDS RES. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; Q00553; RGECGL.
PIR; B23970; B23970.
PIR; S40814; S40814.
ECCGENE; EG10387; GLNL.
SENSORY TRANSDCTION; TRANSFERASE; KINASE; PHOSPHORYLATION; NITROGEN FIXATION; ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROCHA M., VAZQUEZ M., GARCIARRUBIO A., COVARRUBIAS A.A.; GENE 37:91-99(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NISHIO S., MANGO S., REITZER L.J., MAGASANIK BACTERIOL. 160:379-384(1984).
                                01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 6; L
Pred. No. 2.71e+00;
7; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REL. 16, CREATED)
(REL. 16, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
    Ä
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349
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 fqltlh-geryrlaarid 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 44.48;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-24 FROM N.A. MEDLINE; 86031370.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X05173; G41564; -.
EMBL; K02176; G146162; -.
EMBL; L19201; G304974; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
STANDARD;
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                                                                                                              GLNL OR NTRB OR GLNR. ESCHERICHIA COLI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                      ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 85006814.
UENO-NISHIO S., MAI
                                                                                                                                                                                                                               STRAIN-K12; MEDLINE; 87174797.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
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ID ITA3 CRISP
AC P17852;
DT 01-NOV-1990 (
DT 01-OCT-1996 (
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NTRB_ECOLI
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GLAGUER M., STIREWALT V.L., BRYANT D.A., SIDLER W., ZUBER H.;
EUR. J. BIOCHEM. 205:927-937(1992).
-!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILLSOMES.
-!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
AND THE LOCATION OF THE DISC-SHAPED PHYCOBILLPROTEIN UNITS WITHIN THE PHYCOBILLSOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ONDER TO MEDIATE A DIRECTED AND OPTIMAL BRREAT PRANSFER.
-!- SUBGNUT: THE PHYCOBILLSOME IS A HEMDISCOIDAL STRUCTURE THAT IS COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
                          - FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
-! FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGREGATION AND THE LOCATION OF THE DISC. SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A DIRECTED AND OFTIMAL ENERGY TRANSFER.
-! SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG3 (L-RC 29.6).
                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 8; Length 252;
Pred. No. 2.71e+00;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 253;
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                                                                                                                                                                                                                         -1- SIMILARITY: TO OTHER PHYCOBILLSOME LINKER PROTEINS. EMBL; M80435; G142102; -. PIR: JS0595; JS0595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO OTHER PHYCOBILLSOME LINKER PROTEINS EMBL; X59763; G44401; -. PIR; S16060; S16060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASTIGOCLADUS LAMINOSUS (FISCHERELLA SP.).
PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); STIGONEMATALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 253 AA; 29493 MW; 820A835D CRC32;
                                                                                                                                                                                                                                                                                   PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY INII_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68; DB 8; L. Pred. No. 2.71e+00; 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                           0C1A6468 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                         252 AA; 29191 MW;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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SEQUENCE FROM N.A.
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969 96
1051 AA;
    EUTHERIA; PRIMATES
                                                                                                                                                                                                        SEQUENCE OF 33-46.
MEDLINE; 87204112.
                                                                                                                               TISSUE=FIBROBLAST
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ID RFAF_HAEIN
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TRANSMEM
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                                                                                                                                    TISSUE-IRROLARS, 90216739.

A SCHARLY, HAKOMORIS.-I., MIURA Y., TAKIO K., TITANI K., PAWAR S., ASAWA T., HAKOMORIS.-I., 10.21

J. BIOL. CHEM. 265:7016-7021(1990).

-I. SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS COMPOSED OF AN HERVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND. ALPHA-3 ASSOCIATES WITH BETA-1.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. STAFFACE RECEPTOR.

-I. SUBCELLULAR AND LINTEGRIN, TRANSMEMBRANE; SIGNAL; INTEGRIN;

-I. STERCELLULAR WATRIX; CYTOSKELETON; REPERT.
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INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA
CHAIN) (CD49C).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                              CRICETIDAE SP. (HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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Pred. No. 2.71e+00;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    HEAVY CHAIN (POTENTIAL).
LIGHT CHAIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
7 X APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336B3FE0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     INTEGRIN ALPHA-3.
                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE TISSUE=FIBROBLAST;
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POTENTIAL.
POTENTIAL.
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Best Local Similarity 37.5%;
Matches 6; Conservative
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| YRLAIRLNERYRLAIR 16
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1051 AA;
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CARBOHYD
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-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: WITH OTHER ALPHA CHAINS FROM THE INTEGRIN FAMILY OF EXLL-STRAGE RECEPTOR.
EMBL; D01038; G220141; -.
PIRS: JX0161: JX0161.
PROSITE: PS00242: INTEGRIN_ALPHA.
EXELLA ADHESION: GLYCOPROTEIN: TRANSMEMBRANE; SIGNAL; INTEGRIN;
EXTRACELLULAR MATRIX; CYTOSKELETON; REPEAT.
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SEQUENCE FROM N.A.
MEDLINE; 92011866.
TAKADA Y., MURPHY E., PIL P., CHEN C., GINSBERG M.H., HEMLER M.E.;
J. CELL BIOL. 115:257-266(1991).
                                                                                                                                                                                                                                                              TAKADA Y., STROMINGER J.L., HEMLER M.E.;
PROC. NATL. ACAD. SCI. U.S.A. 84:3239-3243(1987).
-!- FUNCTION: VLA-3 ACTS A RECEPTOR FOR FIBRONECTIN, LAMININ AND
COLLAGEN.
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Pred. No. 2.71e+00;
6; Mismatches 3; Indels
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HEAVY CHAIN (POTENTIAL).
LIGHT CHAIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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7 X APPROXIMATE REPEATS.
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                                                                                                                                                 MEDLINE; 91331981.
ISUJI T., HAKOMORI S.-I., OSAWA T.;
J. BIOCHEM. 109:659-665(1991).
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                                                                                                         SEQUENCE OF 33-1051 FROM N.A.
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Best Local Similarity 43.8%;
Matches 7; Conservative
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STRAIN=LT2;
KUSTU S.G.;
KUSTU S.G.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
NITROGEN LEVEL OF CELL AND MODULARES THE ACTIVITY OF WITC.
INTROGEN LIMITATION NIRB ACTIVATES NTRC BY PHOSPHORYLATING IT,
WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
INACTIVATED BY NTRB.

-!- SIMILARITY TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
KINASES.
                                                                        SALMONELLA TYPHIMURIUM.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACILLUS THURINGIENSIS (SUBSP. ISRAELENSIS).
PROKARYOTA, FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89008093.

DONOVAN W.P.,

J. BACTERIOL. 170:4732-4738(1988).

J. BACTERIOL. 170:4732-4738(1988).

J. BACTERIOL. 170:4732-4738(1988).

EUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF MOSGUITOS.

J. POXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

J. DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
72 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-).
THE (BY SIMILARITY).
FEAGE4028 CRC32;
                                                                                                                                                                                                                                                                                                                                                EMBL; X85104; G728723; -.
STYGENE; SG10569; NTRB.
SENSORY TRANSDOCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
NITROGEN FIXATION; ATP-BINDING.
DOMAIN 116 349 PHOSPHORYLATION (AUTO.).
MOD_RES 139 139 PHOSPHORYLATION (AUTO.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 6; Length 349;
Pred. No. 7.24e+00;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
GLNL OR NYRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 2; L
Pred. No. 7.24e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72348 MW; 0C528C2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA; 38443 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 fqltlh-geryrlaari 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|::: |||||| |:
1 YRLAIRLNERYRLAIRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M31737; G142763; -. PIR; A43647; A43647. TOXIN; SPORULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 ykliirvrvpyrlp 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                            329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLAIRLNERYRLA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE SPORE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 AA;
                                                                                                            ENTEROBACTERIACEAE
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ur 12
CR72_BACTI
P21256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTOXIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                TERRINED / KWACO.

MEDLINE, 95350630.

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D.,

SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,

WITERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 11; Length 424;
Pred. No. 3.77e+00;
8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 8; Length 346;
Pred. No. 3.77e+00;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 48.0 KD PROTEIN F10B5.5 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL). 
9C8A7686 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPOPOLYSACCHARIDE BIOSYNTHESIS; TRANSFERASE. SEQUENCE 346 AA; 38847 MW; 1B4C2E89 CRC32;
                 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ADP-HEPTOSE--LPS HEPTOSYLITRANSFERASE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 186 A
424 AA; 48022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTRB_SALTY STANDARD;
P41788;
01-NOV-1995 (REL. 32, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.5%;
larity 52.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vuery Match
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 hlsirmndkysksvmle 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 yrlgkslregydmaivl 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLAIRLNERYRLAIRLN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIRLNERYRLAIRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F10B5.5.
CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                         RFAF OR HI1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YQQ5_CAEEL
Q09535;
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Query Match

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Matches

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Gaps

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Gaps

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RESULT

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T; REPEAT; ZINC-FINGER; ISOMERASE; ROTAMASE.
RANBEL-LIKE.
C4-TYPE.
                                 JOHNSTONE I.L., MCCABE P.C., GREAVES P., GURR S.J., COLE G.E.,
BROW M.A.D., UNKLES S.E., CLUTTERBUCK A.J., KINGHORN J.R., INNIS M.A.,
GENE 90:181-192(1990).
-!- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
-!- CAȚALYTIC ACTIVITY: 3 NAD(P)H + NITRITE = 3 NAD(P)(+) + NH(4)OH +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95294031.

WU J., MATURIZ M.J., KRAEMER D., BLOBEL G., COUTAVAS E.;

J. MATURIZ M.J., KRAEMER D., BLOBEL G., COUTAVAS E.;

J. BIOL. CHEM. 270:14409-14213(1995).

-!- FUNCTION: INVOLVED IN TRANSPORT FACTOR (RAN-GTP, KARYOPHERIN)-

MEDIATED PROPERIN IMPORT VIA THE F-G REPEAT-CONTAINING DOMAIN

WHICH ACTS AS A DOCKNIG SITE FOR SUBSTRATES. COULD ALSO HAVE

ISOMERASE OR CHAPERONE ACTIVITY AND MAY BIND RNA OR DNA.

-!- SUBSTLATATES LOCATION: NUCLEAR PORE COMPLEX. CYTOPLASMIC FILAMENTS.

-!- SIMILARITY: CONTAINS AND X-X-F-G REPEATS.

-!- SIMILARITY: CONTAINS A RANBP!-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS A CYCLOPHILIN-LIKE PPIASE DOMAIN.

EMBL: L41840; G857368; -

NUCLEAR PROTEIN; TRANSPORT; REPEAT; ZINC-FINGER; ISOMERASE; ROTAMASE.
                                                                                                                                                -!- SUBUNIT: HOMODIMER.
-!- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS
A SIROBEME AND ONE ZFE-2S IRON-SULFUR CENTER.
-!- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-45/SIROHEME DOMAIN
FOUND IN NITRIFE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.7.7.1).
EMBL; MS2029; G168064; -.
PIR; JH0181; JH0181.
PROSITE; PS00365; NI_SIR.
OXIDOREDUCTASE; FAD; FLAVOPROTEIN; IRON-SULFUR; NITRATE ASSIMILATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 6; Length 1104;
Pred. No. 9.99e+00;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               FAD (POTENTIAL).
NAD(P)H (POTENTIAL).
IRON-SULFUR (ZFE-2S) (1
IRON-SULFUR (ZFE-2S) (1
IRON-SULFUR (ZFE-2S) (1
IRON-SULFUR (ZFE-2S) (4
IRON-SULFUR (ZFE-2S) AM; 74485174 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1104 AA; 122731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736 mairlegryk-sir 748
                                                                                                                                                                                                                                                                                                                                                                   720
720
726
760
760
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LAIRLNERYRLAIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOPORIN) (P270).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
                     MEDLINE; 90382664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 15
N358_HUMAN
P49792;
                                                                                                                                                                                                                                                                                                                                                 HEME; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   m
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                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
MEDLINE, 88131318.
MEDLINE, 88131318.
POWELL P.P., KYLE J.W., MILLER R.D., PANTANO J., GRUBB J.H., SLY W.S.;
BIOCHEM. J. 250:547-555(1988).
-!- FUNCTION: BETH-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE
DEGRADATION OF DERMATAN AND KERATAN SULFATES.
-!- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
ALCOHOL + D-GLUCURONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEAR ITS
KD. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TASSUE-PREPUTIAL GLAND;
MEDILINE; 87016933.
NISHIMURA Y., ROSENFELD M.G., KREIBICH G., GUBLER U., SABATINI D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: HOMOTETRAMER.
-i- SUBLILIAR LOCATION: LYSOSOMAL.
-i- SUBCELLULAR LOCATION: LYSOSOMAL.
-i- SUBCELLULAR LOCATION: LYSOSOMAL.
-i- SUBCELLULAR SA POSTRAMSCEN PROTEOLYTIC CLEAVAGE NOT ELEMANAL END. WHICH REDUCES ITS SIZE BY APPROXIMATELY 3 RITE OF THIS CLEAVAGE HAS AS YET NOT BEEN DETERMINED.
-i- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
EMBL; M13962; G204330; -.
EMBL; Y00717; G788260; -.
PIR; A25047; A25047.
                                                                                                                                                                   EUKARYOTA; METAZOA; CHÖRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-GLUCURONIDASE.
PROTON DONOR (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S00345; S00345.
PROSITE; PS00608; GIXCOSYL_HYDROL_F2_2.
PROSITE; PS00719; GIXCOSYL_HYDROL_F2_1.
HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                           ADESNIK M., ANDY R.;
PROC. NATL. ACAD. SCI. U.S.A. 83:7292-7296(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> E (IN REF. 2).
V -> L (IN REF. 2).
M -> L (IN REF. 2).
V; AF91C615 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 1; L
Pred. No. 9.99e+00;
                                                   01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                   648 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NITRITE REDUCTASE (NAD(P)H) (EC 1.6.6.4).
                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 14-648 FROM N.A.
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Best Local Similarity 23.5%;
4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 ywisvqgsdhfqlevrl 261
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| YRLAIRLNERYRLAIRL 17
                   STANDARD;
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                                                                                                                                                   RATIUS NORVEGICUS (RAI)
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NIR_EMENI
P22944;
IT 13
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P06760:
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3224 AA

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Gaps

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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

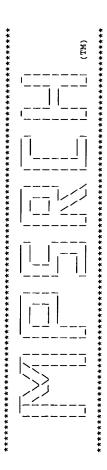
RANBP1-LIKE.	RANBP1-LIKE.	RANBP1-LIKE.	PPIASE, CYCLOPHILIN-TYPE.	MW; 113D9513 CRC32;
2142	2439	3040	3224	AA; 358214
2013	2310	2912	3063	3224
DOMAIN	DOMAIN	DOMAIN	DOMAIN	SEQUENCE
FT	FT	FI	FI	ÖS

Query Match 41.6%; Score 64; DB 6; Length 3224; Best Local Similarity 44.4%; Pred. No. 9.99e+00; , Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps Db 166 hunirlvevyrstkrlkd 183 :: || | | | : ||:: Qy 2 RLAIRLNERYRLAIRLNE 19

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Search completed: Thu May 22 08:34:19 1997 Job time: 12 secs.

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of Edinburgh, U.K. Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc. protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:37:03 1997; MasPar time 2.04 Seconds 64.216 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-36 (1-12) from US08653294.pep 98

YRLAIRRIALRY 12 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

i.parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 a-geneseq26

Mean 19.057; Variance 63.971; scale 0.298 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	8	ဗု	5	5	102	£05	<sup>+</sup> 02	<del>1</del> 02	102	£05	502	102	F02	502	502	502	502	502	502	102	502
	Pred. No	.346-03	1.74e+01	61e+01	02e+02	02e+02	02e+02	02e+02	27e+02	27e+02	27e+02	27e+02	27e+02	27e+02	27e+02	27e+02	27e+02	57e+02	57e+02	57e+02	94e+02
	Pr	7	H	9	4	H	ä	H	ä	ä	H	4	ςi,	H	H	ä	H	H	۲.	H	Η.
	Description	HLA-B2702 84-79-84 pa	Human MHC 1 alpha 1 d	DNA-ligase-III.	Brevibacterium flavum	Enzyme M-11.	Yeast MSH1 protein.	Yeast MSH1 protein wi	HLA-B2702 CTL modulat	HLAB38.6084.	Peptide fragment of H	HLAB38 CTL modulating	Sequence of HLA-B51 a	HLA-Bw53 exon.	Sequence of HLA-Bw52	Alpha 2 subunit of a	Chloroperoxidase.	Type I ribosome-inact	pJH1 gene product - b		
	日	R95429	R71429	R95634	R28073	R79949	R76066	R76070	R92911	R95422	R48286	R83093	R03144	R12463	R03142	R73966	R82249	R74182	R04104	R44431	R95415
	DB	18	13	18	'n	12	14	14	16	18	ထ	16	7	m	7	14	12	14	Н	ω	18
	Query Match Length	12	18	911	334	772	959	971	20	25	25	25	362	362	362	529	640	263	939	3567	20
æ	Query	100.0	62.2	56.1	54.1	54.1	54.1	54.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	52.0	52.0	52.0	51.0
	Score	86	61	55	53	53	53	53	52	25	25	52	52	25	25	25	52	51	51	21	20
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1.94e+02 1.94e+02 1.94e+02 1.94e+02			2.40e+02 2.40e+02 2.40e+02 2.40e+02	2.40e+02 2.40e+02 2.40e+02 2.40e+02	2.40e+02 2.40e+02 2.40e+02 2.40e+02	4.4
HLA-B7 CTL modulating fbp2, for reverse gen 3-acylating enzyme. Virulence gene cluste	5-84 x of gmen	2 84-75-84 a virus typ 2.60-84.	Peptide fragment of C HLA-B2702 CTL modulat Synthetic alpha-trich Mature alpha-Trichosa	Type I ribosome-inact Trichosanthin from Tr Trichosanthin from Tr Trichosanthin protein	ese cu santhi ostati idnev	Polycystic kidney dis Polycystic kidney dis
R92913 R46556 R49828 R97246	R95425 R95413 R41208 B95430	R95428 R05012 R95416	R41205 R83090 R07518 R25573	R74181 R07514 R25572 R29272	R32986 R55129 R39264 W00870	6.9
16 19	1 8 18	18 78	27	4.220	10 70	15
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				20.00		
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222 232 432	2 2 2 2 2 2 2 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	999	ა ღ ო ო გ ო 4 დ	9 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 3 2 1 0	44 45

### ALIGNMENTS

PP 18-MAY-1995.

PP 10-NOV-1994; U12985.

PP 10-NOV-1994; U12985.

PP 10-NOV-1994; U12985.

PR 10-NOV-1995; US-15040.

PR 10-NOV-1996; US-15040.

PR 10-NOV-R95429;
12-NOV-1996 (first entry)
HIA-B2702 84-79-84 palindrome.
HIA-B2702 84-79-84 palindrome.
HIA: p74; alphal.helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; mix the extracellular portion of p74, in an with p74 for the binding of the p74 ligand. Sequence 12 AA; cytolysis, antigen presenting cell. Synthetic. W09513288-A1. n 1 R95429 standard; peptide; 12 AA. 

Query Match 100.0%; Score 98; DB 18; Length 12; Best Local Similarity 100.0%; Pred. No. 2.34e-03;

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Gaps

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ligase-specific antibodies against it may be used as diagnostic agents for cancer, immunosuppression, hypersensitivity to DNA-damaging agents, etc. A DNA-ligase-antagonist protein may be used in therapy of these conditions, and DNA encoding the antagonist may be used in gene therapy.

Sequence 911 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA fragment contg. corynebacterium biotin synthetase gene used to produce biotin synthetase with high efficiency Claim 6; Page 3; 20pp; Japanese.

The bioB gene from B flavum MJ-233 can be inserted into a plasmid and used to transform host microorganisms for increased production of biotin synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding enzyme reduces amylaceous saccharide to produce
                                                                                                                       Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 5; Length 334;
Pred. No. 1.02e+02;
4; Mismatches 3; Indels
                                                                                                                       Score 55; DB 18; Length 911 Pred. No. 6.61e+01; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 502..506
//note= "used for production of probe sequence (T04206)"
Misc_difference 621..625
/note= "used for production of probe sequence (T04207)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme; M.11; Q36; rhizobium; arthrobacter; trehalose; amylaceous saccharide.
 The DNA, protein and
                                                                                                                                                                                                                                                                                                         26-MAR-1993 (first entry)
Brevibacterium flavum MJ-233 biotin synthetase.
Bloobs, ss.
Brevibacterium flavum MJ-233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsusaki
                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1991; 062563.
04-MAR-1991; DP-062563.
(MITP ) MITSUBLSHI PETROCHEMICAL CO LTD.
WPI; 92-377571/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Kubotca M, Maruta K, Sugimoto T, T
WPI: 95-329870/43.
N-PSDB; T04155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                   r 4
R28073 standard; Protein; 334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
 relaxation of supercoiled DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 772
                                                                                                                       56.1%;
|larity 54.5%;
|Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 54.1%;
Local Similarity 41.7%;
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1995; 301176.
23-FEB-1994; JP-047956.
23-FEB-1994; JP-047940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-1994; JP-090728.
06-APR-1994; JP-090705.
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1 YRLAIRRIALRY 12
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                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                               2 RLAIRRIALRY 12
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                                                                                                                                                                                                                                                                                                                                                                                       02-0CT-1992
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                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                              R28073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 5
R79949 a
                                                                                                                                                       Matches
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                                                                                                                                               12-OCT-1995 (first entry)

Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor;

Majora 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation;

arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human DNA ligase III gene - used to develop prods. to treat, prevent or diagnose DNA disorders such as abnormal cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents human DNA-ligase-III from activated T-lymphocytes, and includes a putative signal peptide sequence. DNA-ligase-III is a new protein larger than DNA-ligase-II, and differs from DNA-ligase-I in repairing single-strand breaks in DNA efficiently, but not performing blunt-end joining or AMP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 45; 103pp; English.

7124-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
receptors. Via competitive Inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair;
immunostimulant;
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                                                                                                                                                                                                                                                                          12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALLFORNIA.
Goldstein A. Goodenow RS, Olsson L;
WPI: 95-098577/13.
Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61; DB 13; Length 18;
Pred. No. 1.74e+01;
4; Mismatches 2; Indels
 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-ligase_III.

Human; DNA-ligase-III; activated T-lymphocyte; diagnostic; antibody; immunoassay; antitumour; gene therapy; DNA-ligase-III-antagonist.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 911 AA.
                                                                                                       r 2
R71429 standard; peptide; 18 AA.
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"Putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 MAY-1994; U12922.
08-NOV-1994; U12922.
(HUMA-) HUMAN GENOME SCI INC.
Haseltine WA, Wel Y;
WPI; 96-251747/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.2%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-1996 (first entry)
12; Conservative
                            l yrlairrialry 12
                                                         1 YRLAIRRIALRY 12
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1 YRLAIRRIALRY 12
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W09614394-A1.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                              WO9505189-A.
                                                                                                                                                                                                                                                              23-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                       receptor
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R95634 s
R95634;
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Matches
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R92911;
16-MAY-1996 (first entry)
HIA-B2702 CTL modulating epptide (B2702.84-75/84-75).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 167-171; 256pp; English.

R76070 is the S.cerevisisae mismatch repair pathway protein MSH1, containing the IZCA5 epitope. It is used in the analysis of possible mutations in the human mismatch repair genes. Defects or alterations in such a gene result in the accumulation of unstable repeated DNA sequences, a feature of a number of different cancers. The identification of a defect in the mismatch repair pathway can be particular mammalian cancer e.g colorectal, ovarian, endometrial (uterine), renal, bladder, skin, rectal and bowel. The nuclectide sequences and polypeptides of the hMSH2 gene may also be used for Sequence 971 AA;
                                                                                                                                             16-0AN-1996 (first entry)
Yeast MSH1 protein with I2CA5 epitope tag.
Mismatch repair; MSH2; primer; identification; defect; alteration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining alteration in human mismatch repair pathways - used in the diagnosis, prognosis and therapy of cancers and in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 971;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 14; I
Pred. No. 1.02e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                       26-MAY-1995.
17-NOV-1994; U13385.
17-NOV-1993; US-154792.
07-DEC-1993; US-163449.
13-JUN-1994; US-259310.
(UYVE-) UNIY VERMONT & STATE AGRIC COLLEGE.
(DAND) DANA FARBER CANCER INST.
Fishel R, Kolodner RD, Reenan RAG;
WPI; 95-200377/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                         R76070 standard; Protein; 971 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R92911 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 fr-pisrvslry 21 :: | :: | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krei
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
WO9526979-A1.
12-OCT-1995.
                                                                                                                                                                                                                                                                                                              WO9514085-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assays
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Matches
                                                                                                셤
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Claim 3; Page 21-22: 178pp; English.

This sequence represents an enzyme that forms a non-reducing sugar with a trehalose end group, from a reducing amylaceous saccharide. The analyse of group, from a reducing amylaceous saccharides have a degree of glucose polymerisation of 3 or higher. This sequence was extracted from a liquid culture of Rhizobium of this sequence, the encoding sequence was obtained. The encoding sequence was obtained. The encoding sequence was obtained. The encoding sequence of chis sequence, the encoding sequence was obtained for the DNA encoding enzyme of transformants. This can also be performed for the DNA encoding enzyme of 536 (see T04156), which was obtained from Arthrobacter sp. 036. The CC on-reducing sugars produced by the action of these enzymes can be used to food, cosmetics, pharmaceuticals and feeds. They are used as sweeteners, taste and quality improvers, stabilisers fillers, excipients and adjuvants. The sugars can also be used as intermediates for can adjuvants. The advantages with using these sugars, are that, they are ccc practically non-reducing (so no browning reaction occurs when they are consistly and moisture-retaining properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatch repair; MSH2; primer; identification; defect; alteration; cancer; tumour; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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    useful in foods,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Pred. No. 1.02e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 15; I
Pred. No. 1.02e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1994; U13385.
17-NOV-1993; US-154792.
07-DEC-1993; US-259310.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGES.
(DAND) DANA FARBER CANCER INST.
FISHEL R, KOLOGHER RD; Reenan RAG;
   gp.
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sugar with trehalose end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 6
R76066 standard; Protein; 959 AA.
                      cosmetics, pharmaceuticals, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.1%;
larity 85.7%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fr-pisrvslry 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    feast MSH1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 AA;
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N-PSDB; Q93913.
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R76066;

RESULT

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Sequence Query Match

Best Loca Matches

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Gaps

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12-0CT-1995
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Tomposes. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 9, 29pp. English.

CC R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte antiques on be used to isolate he protein py4 from a T-cell activation in mammalian T-cells, and is also immunologically corress reactive with the heat shock protein Hs70. py4 is found in a corst reactive with the heat shock protein Hs70. py4 is found in a climited number of cell types, but is particularly expressed on B and T cells. py4 can be isolated by lysis of a suitable cell with an compositions comprising the extracellular fragment of py4 combined with compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of determining Them with the extracellular portion of py4 and determining the amount of binding between the candidate componiation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of py4, in an amount sufficient to compete with py4 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                          12-NOV-1996 (first entry)
HIAB38 6084.
HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
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                                                                                                                            Gaps
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ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; KW, parasitic disease; cytotoxic I lymphocyte; modulation.
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                                                                                          Score 52; DB 16; Length 20;
Pred. No. 1.27e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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Pred. No. 1.27e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995,
10-NOV-1994; U12985,
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                      cytolysis; antigen presenting cell. Synthetic. W09513288-A1.
                                                                                                                                                                                                                   LT 9
R95422 standard; peptide; 25 AA.
R95422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.1%;
ilarity 66.7%;
Conservative
                                                                                             Query Match 53.1%;
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krensky AM;
                                                                                                                           8; Conservative
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| YRLAIRRIALRY 12
                                                                                                                                                         1 yrlair-lnery 11
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| YRLAIRRIALRY 12
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Best Local Similarity
                                                                20 AA;
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WPI; 95-194027/25
                                                                Sequence
                                                                                                                            Matches
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EXEMPLE 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
Class I major histocompatibility complex (MHC) antigens. This sequence
corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
HIAB38. These sequences can be used to extend the period of acceptance
by a recipient of a transplant from an MHC unmatched donor. The peptides
are administered to a patient in conjunction with a subtherapeutic amount
of an immunosuppressant. This is administered to the patient for a
limited period of time (compared to the lifetime administration for
current treatments). The peptides particularly modulate (or inhibit) the
sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLAB38 CTL modulating pertide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; Immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLAB38.
                                                                                                                                                                                       Mew peptide(s) Dased on Class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets brample 13; Page 39; 61pp; English.

Example 13; Page 39; 61pp; English.

Example 13; Page 39; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from T-cell composition. This peptide is derived from the HLA-B38 antigen and corresponds to the mainly acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 8; Length 25;
Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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Pred. No. 1.27e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krensky AM, Parham P;
                                                             02-MAR-1992; US-844716.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 11
R83093 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.1%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 66.7%;
Matches 8; Conservative
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16-SEP-1993.
25-FEB-1993; U01758
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05-APR-1995; U04349
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WPI; 95-358582/46.
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Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
11-AUG-1988; JP-200758
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WO9513299-A.
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30-NOV-1995
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                                                                                                                                                                                                 11-AUG-1988; JP-200758.

(OLVU) Olympus Optical Co., Ltd.

Kano K, Takfguchi, M.

WPI; 90-046289/07.

New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.

Disclosure; Pages 12-13; 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIA-BWS3 gene, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc.
Claim 2; Page 1; 11pp; Japanese.
Probes comprising part of the sequence encoding the protein can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-Bw53 antigen. See also J03112485 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I.
MHC; class I.
MHC; class I.
J03112487-A.
14-MAY-1991.
22-SEP-1989; 247697.
22-SEP-1989; D-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
WPISS Q12114.
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Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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Pred. No. 1.27e+02;
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                19-MAR-1991 (first entry)
Sequence of HLA-B51 antigen.
Probe; HLA class I DNA; immunogen.
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19-MAR-1991 (first entry)
Sequence of HLA-BW52 antigen.
Probe; HLA class I DNA; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /T 13
12463:
12463:
29-AUG-1991 (first entry)
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R03142 standard; protein; 362 AA
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66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%;
Similarity 66.7%;
8; Conservative
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| YRLAIRRIALRY 12
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Best Local Similarity
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                                                                                                    Homo sapiens.
EP-354580-A.
14-FEB-1990.
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EP-354580-A.
14-FEB-1990.
10-AUG-1989.
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New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA used to develop prods. for detection, diagnosis and therapy and for modulating activity activity.

Disclosure, Page 43-46; 54pp; English.

Disclosure, Page 43-46; 54pp; English.

DIA encoding the human nNaChR alpha2 subunit was isolated froma human thalama tissue cDNA library using corresp. rat cDNA. The control insert of one clone obtd. was ligated with the insert of another clone to generate a full-length alpha 2 subunit cDNA. The DNA can be used to famentify function nNaChRs. Cells contg. the DNA can be used for screening to identify cpds. Which modulate the activity of human nNaChRs. The human nNAChR alpha 2 subunit can be used to product antibodies which can be used in immunohistochemistry, diagnosis and creating animal models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NoV-1995 (first entry)
Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
Human nNAChr; neuronal nicotinic acetylcholine receptor;
neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Kano K, Takiquchi, M.

Rano K, Takiquchi, M.

New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.

Disclosure; Page 13: 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.27e+02;
1; Mismatches 2; Indels
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Pred. No. 1.27e+02;
3; Mismatches 3; Indels
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08-NOV-19934; U12859.
08-NOV-199394; US-149503.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Elilott K.O., Ellis SB, Harpold MM;
WPI; 95-194036/25.
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R73966 standard; Protein; 529 AA.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:34:36 1997; MasPar time 3.23 Seconds 176.531 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-31 (1-20) from US08653294.pep 154 1 YRLAIRLNERYRLAIRLNER 20 Title: Description: Perfect Score:

Sequence:

Scoring table:

89912 seqs, 28507787 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir50

Mean 28.882; Variance 64.246; scale 0.450 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	1.85e+00	4.43e+00	5.91e+00			1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.04e+01	1.38e+01	2.40e+01	2.40e+01	2.40e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01
Description	cellobiose phosphotr	5-exo-hydroxycamphor	outO protein - Erwin	DNA-directed DNA pol	DNA-directed DNA pol	rod-core linker poly			>	integrin VLA-3 alpha	VLA-3 alpha subunit	ADP-heptose-lps hept	nitrogen regulatory	72K crystal protein	mismatch DNA recogni	hypothetical protein	stylar glycoprotein	beta-glucuronidase (	nitrite reductase (N	nitrite reductase (N	Ran-binding protein
ID	D49898	534613	S32869	S19263	JDEC22	JS0595	S23475	RGECGL	A35761	A40021	I55534	G64182	\$53023	A43647	S62790	I40586	LNNTS6	A25047	PS0299	JH0181	S58884
DB	101	ហ	9	S	<del></del> 1	σ	σ	4	14	13	14	σ	7	10	16	10	Н	Ŋ	12	12	13
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Ouery Match	48.1	46.1	45.5	45.5	45.5	44.2	44.2	44.2	44.2	44.2	44.2	43.5	42.2	42.2	42.2	41.6	41.6	41.6	41.6	41.6	41.6
Score	74	7.1	70	70	70	68	68	68	68	68	99	29	65	65	65	64	64	64	64	64	64
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Erwin         5.91e+           70         45.5         783         1 JDEC22         DNA-directed DNA pol         5.91e+           68         44.2         253         9 150595         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         349         4 RGECGL         glnL regulatory prot         1.04e+           68         44.2         1051         14         345561         cell surface glycopr         1.04e+           68         44.2         1051         14         155534         VLA-3 alpha subunit         1.04e+           68         44.2         1053         14         155534         VLA-3 alpha subunit         1.04e+           67         43.5         34         7 5553023         nitrogen</td><td>Ouery Score Match Length DB ID Description Pred. 74 48.1 245 10 D49898 cellohiose phosphotr 1.8564 75 45.1 245 10 D49898 cellohiose phosphotr 1.8564 76 45.5 779 9 \$32869 outO protein - Erwin 5.9164 70 45.5 783 1 JDEC22 DNA-directed DNA pol 5.9164 68 44.2 253 9 JS0595 rod-core linker poly 1.0464 68 44.2 254 9 \$23475 rod-core linker poly 1.0464 68 44.2 1051 14 A35761 cell surface glycopr 1.0464 68 44.2 1051 14 A35761 cell surface glycopr 1.0464 64 1053 14 I55534 VLA-3 alpha 1.0464 67 43.5 346 9 G64182 ADP-heptose-lps hept 1.3864 65 42.2 349 7 \$53023 nitrogen regulatory 2.4064 65 42.2 643 10 A45647 72K crystal protein 2.4064 65 42.2 818 16 \$652790 nismatch DNA recogni 2.4064</td><td>Query         Query         Description         Pred.           74         48.1         245 10         D49898         cellobiose phosphotr         1.85e+           71         46.1         361         5 334613         5-exo-hydroxycamphor         4.3e+           70         45.5         768         5 319263         DNA-directed DNA pol         5.91e+           70         45.5         783         J DEC22         DNA-directed DNA pol         5.91e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         1051         4 RGECGL         glnL regulatory prot         1.04e+           68         44.2         1051         4 A022         1 Integrin VL-3 alpha         1.04e+           68         44.2         1051         4 A021         Integrin VL-3 alpha         1.04e+           68         44.2         1053         4 E55534         ADP-heptose-lps hept         1.38e+           65         42.2         349         7 S53023         nitrogen regulatory         2.40e+           65         42.2</td><td>Query         Score         Match Length DB         ID         Description         Pred.           74         48.1         245 10         D49898         cellobiose phosphotr         1.85e+           71         46.1         361         5 334613         5-exo-hydroxycamphor         4.43e+           70         45.5         788         5 32869         0utO protein - Erwin         5.91e+           70         45.5         783         1 JDEC22         DNA-directed DNA pol         5.91e+           68         44.2         253         9 150595         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         1051         14         RGECGL         glnL regulatory prot         1.04e+           68         44.2         1051         14 A35761         cell surface glycopr         1.04e+           68         44.2         1053         14 155534         VLA-3 alpha submit         1.04e+           67         42.2         346         9 G64182         ADP-heptose-lps hept         1.38e</td><td>Ouery Score Match Length DB ID Description Pred. 74 48.1 245 10 D49998 cellobiose phosphotr 1.8564 75 45.1 245 10 D49998 cellobiose phosphotr 1.8564 76 5 534613 5-exo-hydroxycamphor 4.4367 70 45.5 768 5 S192869 OutO protein - Erwin 5.9164 70 45.5 783 1 JDEC22 DNA-directed DNA pol 5.9164 44.2 253 9 JOS095 rod-core linker poly 1.0464 44.2 254 9 S24475 glnL regulatory prot 1.0464 44.2 1051 14 A35761 cell surface glycopr 1.0464 44.2 1051 13 A40021 integrin VLA-3 alpha 1.0464 44.2 1053 14 155534 ADP-heptose-lps hept 1.3864 65 42.2 64.3 10 A43647 72K crystal protein 2.4064 65 42.2 64.3 10 A43647 72K crystal protein 3.1564 41.6 85 11 INNTS6 beta-qlucuronidase (3.1564 41.6 64.1 1.1 INNTS6 beta-qlucuronidase (3.1564 3.1564 1.1 INNTS6 beta-qlucuronidase (3.1564 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.</td><td>Ouery Score Match Length DB ID Description Pred. 146.1 245 10 D49898 cellobiose phosphotr 1.858+1 46.1 245 10 D49898 cellobiose phosphotr 1.858+1 5.279 9 S32869 outO protein - Erwin 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1</td><td>Ouery Score Match Length DB ID Description  74 48.1 245 10 D49898 cellobiose phosphotr 1.85e+ 75 46.1 245 10 D49898 cellobiose phosphotr 1.85e+ 76 45.5 768 5 S19269 DNA-directed DNA pol 5.91e+ 77 45.5 768 5 S19269 DNA-directed DNA pol 5.91e+ 78 41.2 253 9 JS0595 rod-core linker poly 1.04e+ 68 44.2 254 9 S23475 rod-core linker poly 1.04e+ 68 44.2 1051 14 A35761 cell surface glycopr 1.04e+ 68 44.2 1051 14 A35761 cell surface glycopr 1.04e+ 68 44.2 1051 13 A40021 integrin VLA-3 alpha 1.04e+ 67 43.5 346 9 G64182 ADP-heptose-lps hept 1.38e+ 67 42.2 349 7 S53023 nitrogen regulatory 2.40e+ 65 42.2 643 10 A43647 72K crystal protein 2.40e+ 64 41.6 215 1 LNNTS6 stylar glycoprotein 3.15e+ 64 41.6 215 1 LNNTS6 stylar glycoprotein 3.15e+ 64 41.6 771 12 PS0299 nitrite reductase (N 3.15e+ 64 41.6 1104 12 JH0389 nitrite reductase (N 3.15e+</td></td<>	Query         Score         Match Length DB         ID         Description         Pred.           74         48.1         245 10         D49898         cellobiose phosphotr         1.85e+           71         46.1         361         5 334613         5-exo-hydroxycamphor         4.43e+           70         45.5         768         5 32869         0utO protein - Erwin         5.91e+           70         45.5         783         1 JDEC22         DNA-directed DNA pol         5.91e+           68         44.2         253         9 150595         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         349         4 RGECGL         glnL regulatory prot         1.04e+           68         44.2         1051         14         345561         cell surface glycopr         1.04e+           68         44.2         1051         14         155534         VLA-3 alpha subunit         1.04e+           68         44.2         1053         14         155534         VLA-3 alpha subunit         1.04e+           67         43.5         34         7 5553023         nitrogen	Ouery Score Match Length DB ID Description Pred. 74 48.1 245 10 D49898 cellohiose phosphotr 1.8564 75 45.1 245 10 D49898 cellohiose phosphotr 1.8564 76 45.5 779 9 \$32869 outO protein - 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Erwin         5.91e+           70         45.5         783         1 JDEC22         DNA-directed DNA pol         5.91e+           68         44.2         253         9 150595         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         254         9 523475         rod-core linker poly         1.04e+           68         44.2         1051         14         RGECGL         glnL regulatory prot         1.04e+           68         44.2         1051         14 A35761         cell surface glycopr         1.04e+           68         44.2         1053         14 155534         VLA-3 alpha submit         1.04e+           67         42.2         346         9 G64182         ADP-heptose-lps hept         1.38e	Ouery Score Match Length DB ID Description Pred. 74 48.1 245 10 D49998 cellobiose phosphotr 1.8564 75 45.1 245 10 D49998 cellobiose phosphotr 1.8564 76 5 534613 5-exo-hydroxycamphor 4.4367 70 45.5 768 5 S192869 OutO protein - Erwin 5.9164 70 45.5 783 1 JDEC22 DNA-directed DNA pol 5.9164 44.2 253 9 JOS095 rod-core linker poly 1.0464 44.2 254 9 S24475 glnL regulatory prot 1.0464 44.2 1051 14 A35761 cell surface glycopr 1.0464 44.2 1051 13 A40021 integrin VLA-3 alpha 1.0464 44.2 1053 14 155534 ADP-heptose-lps hept 1.3864 65 42.2 64.3 10 A43647 72K crystal protein 2.4064 65 42.2 64.3 10 A43647 72K crystal protein 3.1564 41.6 85 11 INNTS6 beta-qlucuronidase (3.1564 41.6 64.1 1.1 INNTS6 beta-qlucuronidase (3.1564 3.1564 1.1 INNTS6 beta-qlucuronidase (3.1564 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.	Ouery Score Match Length DB ID Description Pred. 146.1 245 10 D49898 cellobiose phosphotr 1.858+1 46.1 245 10 D49898 cellobiose phosphotr 1.858+1 5.279 9 S32869 outO protein - Erwin 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1 5.918+1	Ouery Score Match Length DB ID Description  74 48.1 245 10 D49898 cellobiose phosphotr 1.85e+ 75 46.1 245 10 D49898 cellobiose phosphotr 1.85e+ 76 45.5 768 5 S19269 DNA-directed DNA pol 5.91e+ 77 45.5 768 5 S19269 DNA-directed DNA pol 5.91e+ 78 41.2 253 9 JS0595 rod-core linker poly 1.04e+ 68 44.2 254 9 S23475 rod-core linker poly 1.04e+ 68 44.2 1051 14 A35761 cell surface glycopr 1.04e+ 68 44.2 1051 14 A35761 cell surface glycopr 1.04e+ 68 44.2 1051 13 A40021 integrin VLA-3 alpha 1.04e+ 67 43.5 346 9 G64182 ADP-heptose-lps hept 1.38e+ 67 42.2 349 7 S53023 nitrogen regulatory 2.40e+ 65 42.2 643 10 A43647 72K crystal protein 2.40e+ 64 41.6 215 1 LNNTS6 stylar glycoprotein 3.15e+ 64 41.6 215 1 LNNTS6 stylar glycoprotein 3.15e+ 64 41.6 771 12 PS0299 nitrite reductase (N 3.15e+ 64 41.6 1104 12 JH0389 nitrite reductase (N 3.15e+

7.04e+01	retinograscoma-assoc CYC1/CYP3 transcript	RGBYH1	u 4.	1502		61	4 4 5	
7.04e+01	probable inorganic p MPL-P protein precur	854051 A45266	13	635	30.0 0.0	19	4 4	
7.04e+01	MPL-K protein precur	B45266 S54061	13	579	თ თ	61	41	
7.04e+01	envelope protein - s	⋖ .	16	372	σ,	61	0.4	
7.04e+01	beta-galactoside alp	B56392	14	354	ď	61	39	
7.04e+01	3'-phosphoadenosine	S34193	Ŋ	239	e,	61	38	
7.04e+01	hypothetical protein	G64386	10	108	6	61	37	
	TvB protein - yeast	569842	17	1547	; ;	62	36	
5.40e+01	nitrite reductase -	A49848	12	1176	٠ ذ	62	34	
•	hypothetical protein	S43275	16	1155	ö	62	33	
	protein -	564251	12	818	ö	62	32	
	RNA 10 protein - ric	MWXRRT	4	558	6	62	31	
4.136+01	hypothetical protein	815010	ب م	3165	4. 4 0. 6 0. 6	5 C	7 6	
٠	alpha-amylase (EC 3.	A49512	10	649	ö	93	28	
4.13e+01	development-specific	A30814	14	597	ö	63	27	
4.13e+01	glycoprotein gp13 pr	B45343	4	485	ö	63	26	
4.13e+01	E protein -	S24418	œ	261		63	25	
4.13e+01	Sil protein - Chaco	S43774	16	245		63	24	
4.13e+01	hypothetical protein	E36811	ω	115		63	23	
3.15e+01	nucleoporin Nup358 -	A57545	13	3224	41.6	64	22	

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dehydrogenase gene on the CAM plasmid of Pseudomonas putida (ATCC 17453).
S34613
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#length 361 #molecular-weight 38377 #checksum 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reeves, P.J.; Whitcombe, D.; Wharam, S.; Gibson, M.; Allison, G.; Bunce, N.; Barallon, R.; Douglas, P.; Mulholland, V.; Stevens, S.; Walker, D.; Salmond, G.P.C. Mol. Microbiol. (1993) 8:443-456 Molecular cloning and characterization of 13 out genes from Erwinia carotovora subspecies carotovora: genes encoding members of a general secretion pathway (GSP) widespread in §12869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain long-chain alcohol dehydrogenase homology #label
                                                                                                                                          #authors Koga, H.; Aramaki, H.; Yamaguchi, E.; Takeuchi, K.; Horiuchi,
T.; Gunsalus, I.C.
#journal J. Bacteriol. (1986) 166:1089-1095
#title camk, a negative regulator locus of the cytochrome P-450-cam
hydroxylase operon.
#cross-references MUID:86223770
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outO protein - Erwinia carotovora subsp. carotovora
#formal_name Erwinia carotovora subsp. carotovora
08-bec-1993 #sequence_revision 26-Jul-1996 #text_change
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this sequence has been revised in reference S34613
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#superfamily alcohol dehydrogenase; long-chain alcohol
dehydrogenase homology
NAD; oxidoreductase; zinc
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Best Local Similarity 47.4%; Pred. No. 4.43e+00;
Matches 9; Conservative 4; Mismatches 6; Indels
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##note the nucleotide sequence was submitted
Library, December 1992
                                                                        #fresidues 1-361 ##label ARA
##experimental_source PpG1; ATCC 17453; CAM plasmid
**CE A29844
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#authors Chen, H.; Sun, Y.; Stark, T.; Beattie, W.; Moses, R.E.
#journal DNA Cell Biol. (1990) 9:631-635
#title Nucleotide sequence and deletion analysis of the polB gene of
#scherichia coli.
#cross-references MUID:91083835
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Nucleic Acids Res. (1990) 18:7185-7186
Aphidicolin inhibits DNA polymerase II of Escherichia coll, an alpha-1ike DNA polymerase.
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DNA-directed DNA polymerase (EC 2.7.7.7) II (version 2)
Escherichia coli
#formal_name Escherichia coli
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
19-Oct-1995
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DNA-directed DNA polymerase (EC 2.7.7.7) (version 1)
Escherichia coli
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S15943
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Pred. No. 5.91e+00;
4; Mismatches 4; Indels
  Length 279
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30-Jun-1992 #sequence_revision 30-Jun-1992
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Score 70; DB 9; Len
Pred. No. 5.91e+00;
3; Mismatches 6;
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##residues 'V',2-768 ##label CH2
##cross-references GB:M35371
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##residues 90-768 ##label CHE2
##cross-references EMBL:M35371
NCE A36236
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##residues 1-768 ##label CHE
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Best Local Similarity 50.0%;
Matches 8; Conservative
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##molecule_type DNA
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Proc. Natl. Acad. Scl. U.S.A. (1990) 87:7663-7667
DNA polymerase II sencoded by the DNA damage-inducible dinA
gene of Escherichia coli.
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experimental #label MAT
#length 783 #molecular-weight 90052 #checksum 2286
Mol. Gen. Genet. (1991) 226:24-33
Escherichia coli DNA polymerase II is homologous to
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##residues 2-9,'XQ',12-21,'H',23,'X',25-28 ##label BO2
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Pred. No. 5.91e+00;
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                         alpha-like DNA polymerases.
#cross-references MUID:91238699
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NCE JQ0780
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##molecule_type protein
##residues 2-9 ##label IWA2
                                                             ##molecule_type DNA
##residues 1-783 ##label I
##cross-references EMBL:X54847
ccession S19262
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#accession JQ0780
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Best Local Similarity 50.0%;
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Clauser, M.; Stirewalt, V.L.; Bryant, D.A.; Sidler, W.;
Zuber, H.
Bur. J. Blochem. (1992) 205:927-937
Structure of the genes encoding the rod-core linker
polypeptides of Mastigocladus laminosus phycobilisomes and
functional aspects of the
phycobiliprotein/linker-polypeptide interactions.
$23475
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##molecule_type protein
##residues 2-23 ##label GRY1
##residues 2-23 ##label GRY1
NT Linker polypeptides determine the positions of phycobiliproteins
within the phycobilisome structure.
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##cross-references EMBL:X59763
##note the source is designated as Mastigocladus laminosus
                                                                                                                                            #product rod-core linker polypeptide cpcG4 #status
experimental #label MAT
#length 253 #molecular-weight 29323 #checksum 5904
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            $23475  #type complete rod-core linker polypeptide cpcG3 - Fischerella sp. #formal_name Fischerella sp. 07-Apr-1994 #text_change
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#length 254 #molecular-weight 29624 #checksum
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ntrB regulatory protein
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##residues 1-349 ##label MIR
ENCE S40802
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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S23475; S16060
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1 YRLAIRLNERYRL 13
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| YRLAIRLNERYRL 13
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acts as a signal transducer that responds to the nitrogen level of the cell and modulates the activity of glnG protein; at a low nitrogen level, glnG protein is activated through phosphorylation; at a high nitrogen level, it is deactivated through dephosphorylation at a high nitrogen level, it is struction farmed through dephosphorylation as the superfamily glnL regulatory protein it app binding; regulatory protein; signal transduction #length 349 #molecular-weight 38556 #checksum 8402
Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. (1993) 21:3391-3398
Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.
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cell surface glycoprotein b3 precursor - golden hamster
#formal_name Mesocricetus auratus #common_name golden hamster
12-0ct-1990 #sequence_revision 12-0ct-1990 #text_change
31-Dec-1993
                                                                                                                                                                                                                                                                                                                  Rocha, M.; Vazquez, M.; Garciarrubio, A.; Covarrubias, A.A.
Gene (1985) 37:91-99
Nucleotide sequence of the glnA-glnL intercistronic region of
Escherichia coli.
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##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1993
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J. Biol. Chem. (1990) 265:7016-7021
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#length 1051 #molecular-weight 116455 #checksum
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Pred. No. 1.04e+01;
7; Mismatches 3; Indels (
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Pred. No. 1.04e+01;
7; Mismatches 2; Indels
                                                                                                                                                                                                1-349 ##label PLU
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##residues 1-24 ##label ROC
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#accession A35761
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 37.5%;
Matches 6; Conservative
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1 YRLAIRLNERYRLAIRLN 18
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##residues 1-10
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KEYWORDS
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bb, 574 yslplrmpdrlklgmr 589

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integrin VLA-3 alpha-3 chain precursor - human
fusion regulatory protein FRP2; galactoprotein b3; very late
antigen-3 alpha chain
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#product integrin alpha-3 heavy chain #status predicted
#label CHH\
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DS cell adhesion; duplication; glycoprotein; heterodimer; metal
                                                                                                                                                                                                                                                                    #authors A40021
#authors Takada, Y.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.; Hanler, M.E.
#journal J. Cell Biol. (1991) 115:257-266
#title Molecular cloning and expression of the cDNA for alpha-3 subunit of human alpha-3beta-1 (VLA-3), an integrin receptor for fibronectin, laminin, and collagen.
#accession A40021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tguji, r.; Hakomori, S.; Osawa, r.
J. Blochem. (1991) 109:659-665
Identification of human galactoprotein b3, an oncogenic transformation-induced membrane glycoprotein, as VLA-3 alpha subunit: The primary structure of human integrin
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                                                                                                                                                                                                                   #formal_name Homo sapiens #common_name man
17-0ul-1992 #sequence_revision 17-Jul-1992 #text_change
06-Sep-1996
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The very late antigen family of heterodimers is part superfamily of molecules involved in adhesion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular and biological characterization of fusion regulatory proteins (FRPs): anti-FRP mabs induced HIV-mediated cell fusion via an integrin system.
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##rosidues 33-43,'X',45-49 ##label OHT
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                                                                                                                               #type complete
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##residues 33-1051 ##label TSU
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##cross-references GB:M59911
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#cross-references MUID:87204112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Takeuchi, K.; Hirano, K.; Tsuji, T.; Osawa, T.; Irimura, #journal J. Cell. Biochem. (1995) 57:371-377
#title CDNA cloning of mouse VLA-3 alpha subunit.
#cross-references WID:95279462
#accession I55534
                 #domain transmembrane #status predicted #label TMN\
                                                                                        #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                   VLA-3 alpha subunit - mouse
#formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                           predicted
#length 1051 #molecular-weight 116611 #checksum 8842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1:1053 ##label RES ##cross-references GB:D13867; NID:g220634; CDS_PID:g220635 ##cross-references GB:D13867; Weight 116744 #checksum 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G64182  #type complete
ADP-heptose-lps heptosyltransferase II (rfar) homolog
Haemophllus influenzae (strain Rd KW20)
#formal_name Haemophllus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; nucleic acid sequence not shown;
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                                                                                                                                                               Length 1051;
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Pred. No. 1.04e+01;
7; Mismatches 3; Indels
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                                                                                                                                                               Score 68; DB 13; I Pred. No. 1.04e+01;
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##residues 1-346 ##label TIGR
#label CHL\
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Local Similarity 37.5%;
les 6; Conservative
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Local Similarity 43.8%;
les 7; Conservative
                                                                                                                                                                                                                                        574 yslplrmpdrprlglr 589
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| YRLAIRLNERYRLAIR 16
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##residues 1-109
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                              86,107,265,500,511,
573,605,656,697,
841,857,926,935,
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Donovan, W.P.; Dankocsik, C.; Gilbert, M.P.
J. Bacteriol. (1988) 170:4732-4738
Molecular characterization of a gene encoding a 72-Kilodalton mosquito-toxic crystal protein from Bacillus thuringiensis subsp. israelensis.
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#journal J. Bacteriol. (1989) 171:521-530
#title A 20-kilodalton protein is required for efficient production of the Bacillus thuringiensis subsp. israelensis 27-kilodalton crystal protein in Escherichia coli.
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                                coli
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                         $53023  #type complete nitrogen regulary protein B - Salmonella typhimurium formal_name_Salmonella typhimurium 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 03-May-1996
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##cross-references GB:L42023; TIGR:HI1105
h#note named as homolog to a protein from Escherichia or
type #length 346 #molecular-weight 38847 #checksum 9828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily glnL regulatory protein II
#length 349 #molecular-weight 38443 #checksum 6851
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#length 643 #molecular-weight 72348 #checksum 6237
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72K crystal protein - Bacillus thuringlensis subsp.
israelensis
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submitted to the EMBL Data Library, March 1995
S53023
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Pred. No. 2.40e+01;
6; Mismatches 2; Indels
                                                                                                      Score 67; DB 9; Length 346; Pred. No. 1.38e+01; 3; Mismatches 5; Indels
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##residues 1-643 ##label DON
##cross-references GB:M31737
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##residues 566-643 ##label
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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s62790 #type complete
mismatch DNA recognition protein mutS - Thermus aquaticus
(fragment)
# (fragment)
# (fragment)
23-Aug-1996 #sequence_revision 23-Aug-1996 #text_change
S62790
Takamatsu, S.; Kato, R.; Kuramitsu, S.
Nucleic Acidis Res. (1996) 24-54-640-647
Mismatch DNA recognition protein from an extremely
thermophilic bacterium, Thermus thermophilus HBB.
S62790
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##residues 1-818 ##label TAK
##cross-references EMBL:D63810
RY #length 818 #molecular-weight 91322 #checksum 6755
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Score 65; DB 10; Length 643;
Pred. No. 2.40e+01;
3; Mismatches 4; Indels
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42.2%; Score 65; DB 16; Length 818; Best Local Similarity 52.9%; Pred. No. 2.40e+01; Matches 9; Conservative 3; Mismatches 5; Indels
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Query Match 42.2%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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| YRLAIRLNERYRLA 14
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:35:21 1997; MasPar time 2.19 Seconds 99.340 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-31 (1-20) from US08653294.pep 154 1 YRLAIRLNERYRLAIRLNER 20 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseg26 Database:

|:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19

Mean 19.740; Variance 84.009; scale 0.235 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Pred. No.	6.55e-07	1.33e+00	1.33e+00	3.49e+00	5.10e+00	1.09e+01	1.31e+01	1.58e+01	1.58e+01	2.29e+01	2.29e+01	3.98e+01	3.98e+01	5.73e + 01	5.73e+01	5.73e + 01	5.73e+01	6.86e+01	6.86e+01	6.86e+01
	Description	HLA-B2702 CTL modulat	HLA-B2702 84-75-84 pa	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 84-75T/75-8	HLA-B2702 CTL modulat	E. coli DNA polymeras	E. coli polymerase-II	Human GAP b3 protein.	Hamster GAP b3 protei	Bacillus thuringiensi	67-kD protein toxin.	EHV-4 gC.	Novel intestinal onco	Pyrococcus furiosus a	Sequence encoded by O	T. chalcogramma parti	Transglutaminase (fis	T. chalcogramma trans
	a	R92911	R95428	R92907	R92909	R92908	R95430	R92910	R24441	R70841	R14118	R14117	R97735	P91462	R20796	R30168	R47504	R38889	R65332	R39520	R65302
	DB	16	18	16	16	16	18	16	'n	13	m	ო	18	Н	4	9	σ	ω	17	ω	17
	Match Length DB	20	20	20	20	20	20	20	783	783	1019	1051	643	643	485	597	649	3165	641	641	695
& Query	Match	100.0	53.9	53.9	50.6	49.4	46.8	46.1	45.5	45.5	44.2	44.2	42.2	42.2	40.9	40.9	40.9	40.9	40.3	40.3	40.3
	Score	154	83	83	78	16	72	71	70	70	89	89	65	65	63	63	63	63	62	62	62
Result	No	Н	7	9	4	S	ø	7	80	O	10	11	12	13	14	15	16	17	18	19	20

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Example 15; Page 36; RODP; English.

Example 15; RODP 183096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence.

Example 16; RODP 183096 and R92907-R92914 represent fragments of the class I MHC

Example 16; RODP 183096 and R92907-R92914 represent from an MHC unmatched of a coceptance by a recipient of a transplant from an MHC unmatched donor.

Example 16; RODP 183096 and R92907-R92914 represent to the period of the peptides are administered to a patient in conjunction with a complete for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly of the patient.

Example 18; RODP 183096 and R92907-R9299 and R92909 and R92909 of the patient.

Example 18; RODP 183096 and R92907-R9299 and R92909 and R9
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
(STRD) Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Gaps ö Score 154; DB 16; Length 20; Pred. No. 6.55e-07; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative

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20 20 셤 ŏ RESULT 2 ID R95428 standard; peptide; 20 AA.

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12-0CT-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC R95413, and R95415-7EF, 2012...

CL human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC/0.

CC p74 is found in a limited number of cell types, but is particularly compassed on B and T cells. P74 can be isolated by 1915 of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

CC compositions comprising the extracellular fragment of P74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T Jymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of cT-cells, by combining them with the extracellular portion of P74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition content p74 for the binding of the P74 in an amount sufficient to compete with P74 for the binding of the P74 in an amount sufficient to compete sequence 20 AA;
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
I MHC HLA-B2702. These sequences can be used to extend the period of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996 (first entry)
HIA-B3702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                         12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2704 alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsns. comprising lymphoid surface membrane proteins - which may hinblit cytolytic activity and differentiation of CTLs. Example: Page 12: 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acceptance period of transplants from MHC unmatched using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.33e+00;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                         18-MAX-1995.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                     cytolysis; antigen presenting cell.
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R92907;
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WPI, 95-358582/46.
Extension of acceptance period
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 yrlairlner-renlriair 19
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Best Local Similarity 65.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayberger C, Kr
WPI; 95-194027/25
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WO9526979-A1.
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HAA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                      The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MXY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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116-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HIA-B2702.
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acceptance by a recipient of a transplant from an MHC unmatched donor.
                                                                                                                                                                                                                                                                                                                                              Gaps
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the recipient
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                                                                                                                                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extension of acceptance period of transplants from donor hosts - using Class I B75-84 MHC antigen of
                                                                                                                                                                                                                                                                           Score 83; DB 16; I
Pred. No. 1.33e+00;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krensky AM, Parham P;
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R92909 standard; peptide; 20 AA.
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65.0%;
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65.08;
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05-APR-1994; US-222851.
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05-APR-1994; US-222851
                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                  of the patient.
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N-PSDB; 02544(
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13;
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Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

CK B5443; and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the character of the protein professoriated antigens. This sequence represents the human-leucocyte-associated antigens. These sequences can be used to isolate the protein professoriated with T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell scattain in ammunalian T-cells, and is also immunologically cross reactive with the heat shock protein the scool isolated by lysis of the strong particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound compassion containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount complex composition of p74, for the binding of the p74 ligand.

Sequence 20 AA;
                                                                                                                                                                            Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HIA-B2702 84-7517/75-84T palindrome.
HIA-B2702 84-7517/75-84T palindrome.
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                          Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 5.10e+00;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAX-1195.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytolysis; antigen presenting cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clayberger C, Krensky AM; WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the patient.
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Query Match 46.8%; Score 72; DB 18; Length 20; Best Local Similarity 72.2%; Pred. No. 1.09e+01;

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R892907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuperessant. This is administered to administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                            16-MAY-1996 (first entry)
HIA-B2702 CIL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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Disclosure; Fig 1; 8pp; Japanese.

The sequence is E. coli DNA polymerase II. The DNA encoding this sequence can be introduced into expression plasmids which can then be used to transform cells such that the new polymerase can be collected from the culture on an industrial scale.
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SIRD), CASS (SIRD) AM, FELLING, C. (SIRD), ST 188582/46.
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.31e+01;
1; Mismatches 6; Indels
  Indels
  4;
Mismatches
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08-DEC-1992 (first entry)
E. coli DNA polymerase II.
Expression plasmid; industial production.
Escherichia coli.
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R24441 standard; Protein; 783 AA.
..
                                                                                                                                                                                          R92910 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-0CT-1990; 263125.
02-0CT-1990; JP-263125.
(TAKI ) TAKARA SHUZO CO LTD.
WPI; 92-212759/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%;
Matches 12; Conservative
                                               18
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 yrlatrlner-renlrtalr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIRLNERYRLAIRLNER
                                               1 yrlairlnetrenlrial
                                                                                          1 YRLAIRLNE-RYRLAIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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/label= N-glycosylation
Modified -site 573
                                                                                                                          Modified -site
                                                                                                                                                             Modified -site
                                                                                                                                                                                              Modified -site
                                                                                       Modified -site
 /label= N-glyco
Modified -site
                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                         WO9113983-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                         Domain
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disciosure; Page 28-31; 45pp; English.

The E. coli DNA-polymerase-II (given in R70841) may be engineered by mutagenesis of the encoding DNA (085427) for use with novel combinations of deoxynucleotides and chain-terminating nucleotides in new DNA sequencing protocols. Variants pref. include D156A and/or E158A mutations.
                                                                                                                                                                                                                                               DNA-polymerase; DNA sequencing; 3'-5' exonuclease; replication; enzyme engineering; protein engineering; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variant DNA polymerase(s) for DNA sequencing - having reduced 3'-5' exo:nuclease activity or having enhanced DNA replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70; DB 13; Length 783;
Pred. No. 1.58e+01;
4; Mismatches 4; Indels
   Length 783,
                                    4; Indels
 Score 70; DB 5; Lo
Pred. No. 1.58e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galactoprotein b3; carcinoma; cancer; tumour.
                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      And a state of a state
                                                                                                                                                                                                                                                                                                                                  01-AUG-1994; UO8610.
02-AUG-1993; US-101593.
(UYAL-) UNIV ALBERTA.
(UYSC-) UNIV SOUTHERN CALIFORNIA.
GOOGMAN MF. Reha-Krantz LJ;
NPI: 95-082243/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 10
R14118 standard; Protein; 1019 AA.
R14119 10-DEC-1991 (first entry)
Human GAP b3 protein.
                                                                                                                                                           .T 9
R70841 standard; Protein; 783 AA.
R70841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.5%;
50.0%;
Query Match 45.5%;
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                                                                             31-AUG-1995 (first entry)
                                                                     231 rmlqkhaeryrlplrl 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 rmlqkhaeryrlplrl 246
                                                                                         1: : |||||::||
2 RLAIRLNERYRLAIRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLAIRLNERYRLAIRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= N-glycosylation
Modified -site 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- N-glycosylation
                                                                                                                                                                                                                               E. coli polymerase-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified -site 54
                                                                                                                                                                                                                                                                              Escherichia coli.
WO9504162-A.
09-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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DNA sequences encoding galactoprotein b3 - produced using DNA constructs also antibodies to Gap b3 used to detect tumours that result in alevated expression of protein.

The sequence was deduced from 3 overlapping clones isolated from 5 bisclosure; Fig 6; 46pp; English.

The sequence was deduced from 3 overlapping clones isolated from 5 human T24 cell line cDNA library. The DNA can be used to express the Gap b3 protein which is a transformation-dependent cell surface glycoprotein. The C-terminal 32 AA segment is likely to constitute forming a glycopylated extracellular domain. The N-terminal region has seven homologus repeats, three of which include the putative forming a glycopylated extracellular domain. The alignment of stretch followed by a short (5 AAs) stretch. The alignment of glycine and hydrophobic residues in each repeat shows a similar glycine and hydrophobic residues in each repeat shows a similar the end of most of the longer stretches (except for the 2nd and 7th repeats. The protein may be used to produce antibodies and these, con the DNA sequences, can be used to detect and quantify levels of contain is indicative of certain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 3; Length 1019;
Pred. No. 2.29e+01;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-1991 (first entry)
Hamster GAP b3 protein.
Galactoprotein b3; carcinoma; cancer; tumour.
Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1991.
08-APR-1991; 001606.
12-MAR-1990; US-491910.
(BICM-) BIOMEMBRANE INST.
TSUJI T, YEMMENCE F, HAKOMORI S; WPI: 91-295637/40.
N-PSDB; Q13822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R14117 standard; Protein; 1051 AA.
R14117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 yslplrmpdrprlglr 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |::|: :| ||::|
| YRLAIRINERYRLAIR 16
                                                                                                                                                                                                                                                                            840..841
                                                                                                                                                                                                                                                                                                     Modified -site 894
/label= N-glycosylation
Modified -site 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide 1.32
/label= signal sequence
Cleavage-site 32.33
                                                                                                                      'label N-glycosylation fodified -site 809
                                                                                                                                                                               N-glycosylation
d -site 825
                                                                                                                                                                                                                                                                                                                                                                                               /label= N-glycosylation
Modified -site 937
'label = N-glycosylation
                                                         'label = N-glycosylation
                                                                                                                                                                                                                                            'label- N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label = N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1019 AA;
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PER 04-MAY-1996.

21-MAY-1995.

WAY-1995.

WAY-1996.

WAY-1995.

WAY-1995.

WAY-1996.

WAY-1996.

WAY-1997.

WEAPLIS STATE.

MUTPHY RC.

Stevens SE;

WAPL: 96-259063/26.

WAPL: 
                                                        Bacillus thuringiensis ssp. israelensis CryIVD protein. CryIVD; toxic protein; crystal toxin; expression construct; transformed cyanobacteria; phycocyanin beta; cpcB; promoter; laseticide; dipteran larvae; mosquito; blackfly. Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.2%;
Best Local Similarity 50.0%;
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 ykliirvrvpyrlp 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIRLNERYRLA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 89-263682/36.
N-PSDB; N90712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donovan WP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequences encoding galactoprotein b3 - produced using DNA constructs also antibodies to Gap b3 used to detect tumours that result in elevated expression of protein.

Tresult in elevated expression of protein.

Disclosure; Fig 4; 46pp; English.

The sequence was deduced from 3 overlapping clones isolated from a hamster Nippy cDNA library. The DNA can be used to express the Gap b3 protein which is a transformation-dependent cell surface glycoprotein. The C-terminal 32 AA segment is likely to constitute the cytoplasmic domain with the longer 959 AA residue segment comming a glycopsylated extracellular domain. The protein may be used to produce antibodies and these, or the DNA sequences, can be used to detect and quantify levels of Gap b3 protein or mRNA in contain and contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1051;
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Pred. No. 2.29e+01;
7; Mismatches 3; Indels
                                                   Peptide

33..50

/note= "confirmed by Edman degradation"
Binding-site 315..323

/label= divalent cation binding site
Binding-site 346..354
                                                                                                                                                                                                                                                                                                                                                                                           /label- N-glycosylation
Peptide 544..572
/note- "confirmed by Edman degradation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-glycosylation
Peptide 755..784
/note= "confirmed by Edman degradation"
                                                                                                                                                                                                           Binding-site 406..415
/label- divalent cation binding site Modified -site 468
/label- N-91ycosylation Modified -site 479
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08-APR-1991; U01606.
112-MAR-1990; US-491910.
(BIOM-) BIOMEMBRANE INST.
TSUJ1 T, YAMANOTO F, HAKOMOTI S;
WPI: 91-295637/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jomain 960..987
/label transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
33..1051
mature Gap b3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site 840..841
Modified -site 891
/label= N-glycosylation
Modified -site 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified -site 573
/label= N-glycosylation
Modified -site 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= N-glycosylation
Modified -site 937
/label= N-glycosylation
                                                                                                                                                                                                                                                                                                                                  /label N-glycosylation
Modified -site 541
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Modified -site 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label = N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "confirmed b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1051 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        certain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also R14118
Sequence 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; 013821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9113983-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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Gaps ö

4; Indels

Length 643;

Score 65; DB 18; 1 Pred. No. 3.98e+01; 3; Mismatches

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Bacillus thuringiensis var israelansis cry D toxin gene and proteins used for producing insecticide compsns. active against Dipteran species claim 2; fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Pred. No. 3.98e+01;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                     cryD; Bacillus thuringiensis; biopesticide.
Bacillus thuringiensis var.israelesis.
T 13
P91462 standard; protein; 643 AA.
P91462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                         (first entry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1989;
17-EEB-1989; UO0663.
19-EEB-1988; US-158176.
                                                                                                                                                                                                                                           67-kD protein toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dipteran larvae.
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                                                      ID DAY ONE DAY
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Gaps

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RESULT 12 ID R97735 standard; Protein; 643 AA.

574 yslplrmpdrlklgmr 589

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| | | ::|: :| :|::| | YRLAIRLNERYRLAIR 16

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Search completed: Thu May 22 08:35:34 1997 Job time: 13 secs.
                           Homo sapiens.
                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                          Matches
    쉱
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence (SEQ ID no 2) was deduced from the nucleic acid sequence (SEQ ID no 2) was deduced from the nucleic acid sequence (SEQ ID no 2) was deduced from the nucleic acid sequence obtd. by screening a BamHI library constructed from EVH-4 infected equine dermal cells (NBL-6). The gC protein is homologous to its gC counterpart of other herpesviruses and is characterised by conserved regions within the gC homologues (see feature table). GC cheminal half positioned around six sites of cysteine conservation at residues 256, 318, 357, 361, 390 and 416, in this sequence, implying some degree of conservation of secondary and tertiary structure between gC homologues, presumably involving disulphide bonding. BHV-4 gC has at Asp 409 a site capable of eliciting an immune response. Vaccines derived from this sequence can be prepd., and they may be used to protect horses against EHV-4 infection, other live virus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid sequence encoding \rm EHV-4~gH or gC protein - used to produce a vaccine for protection of horses against \rm EHV-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                  Equine herpes virus-4; glycoprotein gC; antigenic; vaccine; alphaherpesvirus; respiratory disease; cellular attatchment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB 4; Le
Pred. No. 5.73e+01;
2; Mismatches 1;
                                                                                                                                                                                                                                                                    /note= "external domain contg. 11 N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 15
830168 standard, Protein, 597 AA.
830168.
18-MAY-1993 (first entry)
Novel intestinal oncofetal gene product.
                                                                                                                                                                                                                                                                                                                                     /note= "hydrophilic cytoplasmic domain"
Misc-difference 409
                                                                                                                                                               patnoyenio.
Equine herpesvirus-4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       04-JUL-1991, G01091.
6-JUL-1999, GB-14950.
(UNIU ) UNIV OF GLASGOW.
(EQUI-) EQUINE VIROLOGY RES FOUN.
                                                                 T 14
R20796 standard; Protein; 485 AA.
                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain"
Domain 469..485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%;
                                                                                                    19-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                 445..468
                                                                                                                                                                                               Peptide 1..32
//label= signal_peptide
Protein 33..485
544 ykliirvrvpyrlp 557
                                                                                                                                                                                                                                                        33..444
                                                                                                                                                                                                                                                                                                                                                                   "antigenic site"
               Nicolson L, Onions DE; WPI; 92-056872/07.
                                                                                                                                                                                                                                                                                  glycosylation sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= EHV-4_gC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q20995
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Gaps
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oncofoetal; onco-foetal; onco-fetal; intestine; gastrointestinal; cancer; tumour; growth; benign; malignant; neoplasm; metastasis.
                                                                                                                                                                                                                                                                                                                                DNA or RNA molecule encoding intestinal onco-foetal gene - useful for detecting neoplastic cells, esp. intestinally-originating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 597;
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Pred. No. 5.73e+01;
6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                            prim. and metastatic tumours
Claim 1; Fig 8; 12pp; English.
                                                                                                                  15-DEC-1992.
31-AQG-1988; 239084.
31-AQG-1988; US-239084.
(ONTA-) ONTARIO CANCER INST.
Buick RN, Filmus UE;
WPI: 93-008640/01.
N-PSDB; Q33008.
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Local Similarity 46.2%;
les 6; Conservative
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Score 77;
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MEDLINE; 89030641.
MAXER W.E., JONKER M., KLEIN
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EMBO J. 7:2765-2774(1988).
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protein - protein database search, using Smith-Waterman algorithm
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                                                                                                                                                                                                                                                                                                                                                                                                                                               swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
                                                                                                                                                        Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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Listing first 45 summaries
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Perfect Score:
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                                                                                                                                                                                                                                                                                                                                                                                                             CLPB PROTEIN.
DIHVENDELAVOUL-4-RED
CLASS I HISTOCOMPATIB
NUCLECCAPSID PROTEIN.
ENVELOPE POLYPROTEIN
URACIL-DNA GLYCOSYLAS
CBIG PROTEIN.
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PROBABLE SENSOR-LIKE
GLYCOPROTEIN C PRECUR
NUCLEOCAPSID PROTEIN
HEPATOCYTE GROWTH FAC
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INTEGRIN BETA-7 SUBUN
INTEGRIN BETA-7 SUBUN
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CLPB_CORGL
DERA_VITVI
IAO4_GORGO
NCAP_SENDS
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RDGC_DROME
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HGFL_HUMAN
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CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                           01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR (FRAGNENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (FEB-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                       PAN TROGLÓDYTES (CHIMPANZEE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                               .
G
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EMBL; X13115; 6755776; -.

PIR; S03537; S03537.

PIRSP; PO3989; LEA.

PROSTIE: PS00220; IG MAC.

MMC I: TRANSMEMBRANE: GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                               D., IVANYI P., VAN SEVENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 5395FFC9 CRC32;
359
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DB 1; Length 359;

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01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-49(B-21) B*4901.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                          REVISIONS TO 78.
MEDLINE: 93056529.
MELLDERRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E. WILLIAMS R.C., PARHAM P.;
J. IMMUNOL. 149:3563-3568(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. IMMUNOL, 142:306-311(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MADLINE, 89080265.
MATASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E996F82F CRC32;
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MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL
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EMBL; M22799; G553538; JOINED.
EMBL; M22794; G553538; JOINED.
EMBL; M22795; G553538; JOINED.
EMBL; M22796; G553538; JOINED.
EMBL; M22799; G553538; JOINED.
EMBL; M22799; G553538; JOINED.
    J. IMMUNOL. 142:3937-3950(1989).
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X
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nes 10; Conservative
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MIM; 142830; -.
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PIR; B30548; B30548.
HSSP; P03989; IHSA.
MIM; 142830; -.
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362 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RENLRIALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B53_HUMAN
P30490;
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CARBOHYD
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Matches
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE; 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
PROC. NATL. ACAD. SCI. U.S.A. 79:893-897 (1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                              21-JUJ-1986 (REL. 01, CREATED)
01-APR-1993 (REL. 25, LAST SEODENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR (HLA-AR) (HLA-12.4).
                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 77; DB 5; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
Pred. No. 7.49e-02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
5E610F63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
                                                                                                                        362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AA
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                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                       AMER OF ALPHA CHAIN

AMEL, VOO526; GS8683; ALT_INIT.

PIR, A02189; HLHU12.

R HSSP; P03989; 1HSA.

MIM; 142925; -.

MRC TE: Perior.
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206
298
308
332
362
110
283
40850 R
 Best Local Similarity 100.0%;
Matches 10; Conservative
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Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
                                        95 renlrialry 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
362 AA;
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                                                      11 RENLRIALRY 20
                                                                                                          LT 2
HLAH_HUMAN
P01893;
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1B47_HUMAN
P30487;
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DISULFID
SEQUENCE
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TRANSMEM
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW 53 B*3301.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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MEDLINE; 91033941.
HAYASHI H., OOBA T., NAKAYAMA S., SEKIMATA M., KANO K.,
TAKIGUCHI M.;
IMMUNOGENETICS 32:195-199(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
EMBL; MSEGS; G187757; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE; 91067476.
MEDLINE; 9106746.
SAMAI M., GIRDLESTONE J., MILSTEIN C.;
NUCLEIC ACIDS RES. 18:6702-6702(1990).
- I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                     01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANNIGEN, BW-53 B*5301 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOY-1990 (REL. 16, CREATED)
01-NOY-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOY-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
MEDLINE; 90207291.
EDNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4; ZEDC746E CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A45834; A45834.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC I; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLAB.
HOMO SAPIENS (HUMAN)
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P18465;
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TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-AR-1993 (REL. 25, LAST SEQUENCE UPDATE)
CLASS I HISTOCOMPATIBLITY ANYIGEN, 0600-B0101 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
EUKARKOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-52(B-5) B*5201.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
J. EXP. MED. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN; SIGNAL.

BY SIMILARITY.

CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BOILOI ALPHA CHAIN.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.
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Pred. No. 7.49e-02;
......+rhes 0; Indels
                                                                                                                                                                                                                                                                                             Score 77; DB 1; Length 302, Pred. No. 7.49e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
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ZE33E2B8 CRC32;
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3B436FE8 CRC32;
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GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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BY
BY
                                                                                                                                                                                                                                                                     40521 MW;
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                                                                                                                                                                                                                                                                                                            Match 50.0%;
Local Similarity 100.0%;
es 10; Conservative
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Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X60255; G22866; -. PIR; JH0539; JH0539. HSSP; P03989; 1HSA. PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC I; TRANSMEMBRANE;
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309
333
125
227
362 AA;
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                                                                                                                                                                                                                                                                   362 AA;
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1B01_GORGO
P30379;
                                                                                                                     DOMAIN
DOMAIN
TRANSMEM
DOMAIN
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DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                            DISULFID
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TRANSMEM
                                                                                                                                                                                                          CARBOHYD
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAYS J.P., COPPIN H.L., PARHAM P.;
J. BIOL. CHEM. 260:11924-11933(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMOUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA CHAIN BW-58(B-17) B*5801
EXTRACELULAR ALPHA-1.
EXTRACELULAR ALPHA-2.
EXTRACELULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                     Length 362;
                                                                                                                                                                                                                     Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
               ALPHA CHAIN B-27 B*2702.
EXTRACELUJAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; 9798FOBB CRC32;
                                                                                                                      CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                             362 AA
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                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40337 MW;
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PIR; A23895; HLHUB8
HSSP; P03989; HISA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                     Query Match 50.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                       40397
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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2298
3332
332
1110
283
                                 1114
206
208
308
332
362
310
110
1188
283
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SIGNAL 1
                                 25
115
207
209
339
110
125
362 AA;
                                                                                                                                                                                                                                                                                        99 renlrialry 108
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1B62_HUMAN
P10319;
                                                                                    DOMAIN
TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
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DISULFID
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CARBOHYD
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                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-57(B-17) B*5701.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
LOPEZ DE CASTRO J.A.;
PROC. NATL. ACAD SCI. U.S.A. 82:7394-7398(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B*2702 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
 -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                         Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
PARHAM P., ARNETT K.L., ADAMS E.J.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; D91DF8DD CRC32;
                                                                                                                                                                                                                                                                        CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR.1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
PRECURSO HISTOCOMPATIBILITY ANTIGEN, B-27 1
PRECURSOR (B-27K) (B27.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 AA
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                                                                                                                                                      GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 86-107 AND 171-181.
MEDLINE; 86042671.
                                                                                                                                                                                                                                                                                                                                                                         40224 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMENBRANE; GLYCC
                                                               PIR; S12622; S12622.
HR; D35997; D35997.
HSSP: P01989; 1HSA.
MIM; 142830;
PROSITE; PS00299; IG_MHC.
MHC I: TRANSMEMBRANE; GLYC.
                              EMBL; M32318; G307222; -
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125
227
362 AA;
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1B15_HUMAN
P10317:
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                                                                 Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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MEDLINE; 93056508.

MEDLINE; 93056508.

MEDLINE; 93056508.

MEDLINE; 93056508.

MARTGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,

LITLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,

A MARTELL R.W., DU TOIT E.D., PARHAM P.;

J. IMMUNOL. 149:3411-3415(1922).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).

REMBL; X61707; G32187; -.

RISS; P03989; 1HSA.

R HSSP; P03989; 1HSA.

R MIN; 142830; -.

R MIN; 142830; -.

R MIN; 142830; -.

R MIN; 142830; -.

R MIN; ILABNAREMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HARA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2).
                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
IMMUNOGENETICS 29:297-307(1989).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                       -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA CHAIN B-51(B-5) B*5101.
EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 362;
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Pred. No. 7.49e-02;
0; Mismatches 0;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, 4D846F30 CRC32;
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0; M
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M22792 G53533 ALT_SEQ.
M22786 G535333 JOINED.
M22788 G535333 JOINED.
M22788 G535333 JOINED.
M22789 G53533 JOINED.
M22791 G535333 JOINED.
M2791 G53533 JOINED.
M2791 G53533 JOINED.
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JOINED.
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Best Local Similarity 100.0%;
Matches 10; Conservative
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206
208
308
332
362
1110
188
283
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PIR, A30548, A30548.
SSSP, P03989, 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_M
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE;
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362 AA;
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11 RENLRIALRY 20
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P30497;
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TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
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SIGNAL
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EMBL;
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EMBL;
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                                01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CLASS I HISTOCOMPATIBLILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA (LOWLAND GORILLA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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P18464;
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 33, LAST SEQUENCE UPDATE)
10-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
11A CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PPRECIRSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                 MEDLINE; 92078860.

JEMURD D.A., WAREN E., TAYLOR P., PARHAM P.;
J. EXP. MED. 174:1491-1509(1991).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; XGOS24, GAZ870, -.

PIR: JH0541; JH0541.

HSSP; P03989; 118A.
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MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIĞUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               HISTOCOMPATIBILITY ANTIGEN,
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 77; DB 1; Length 362; Pred. No. 7.49e-02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGO-B0103 ALPHA CHAIN
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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MEDLINE; 90207291
BENIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
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NY SIMILARITY.
NY SIMILARITY.
FEA6A941 CRC32;
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 362 AA
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CLASS I HISTO
PRT;
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[3]
SEQUENCE FROM N.A.
MEDLINE: 89233295.
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es 10; Conservative
 STANDARD;
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309
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362 AA;
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                              01-APR-1993
 1B03_GORGO
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Matches 1
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SEQUENCE
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362 AA;
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1A23_HUMAN
P30447;
01-APR-1993 (
                1B02_GORGO
P30380;
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CARBOHYD
SEQUENCE
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
PRECURSOR.
              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-57(B-17) B*5702.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-51(B-5) B*5104.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
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EUKRAKOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                            Score 77; DB 1; Length 362;
Pred. No. 7.49e-02;
0; Mismatches 0; Indels
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Pred. No. 7.49e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J., WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.; NATURE 357:326-329(1992).
                                                                                                                                                          Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

628C2156 CRC32;
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F22F08AB CRC32;
                                                                                                                                      CYTOPLASMIC TAIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA.
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BY
BY
                                                                                                                                                                                                             40342 MW;
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Best Local Similarity 100.0%;
Matches 10; Conservative
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Matches 10; Conservative
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HSSP; P03989; 1HSA.
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362
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227
362 AA;
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P30489;
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DISULFID
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            01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
01-AST I HISTOCOMPATTBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
EUTHERRAYOTA, METAZOA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 92078860.
MEDLINE; 9-7, WARREN E., TAYLOR P., PARHAM P.;
J. EXF. MED. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-B0102 ALPHA CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITTLE'A.-M., MADRIGAL J.A., PARHAM P.;
IMMUNGENETICS 35:41-45(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                               THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1,
7.49e-02;
.hac 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;; 3CF119AD CRC32;
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Pred. No. 7.49e-C
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362 AA
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PRT;
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MEDLINE; 92104637.
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Local Similarity 100.0%;
les 10; Conservative
                                                                                                                                                                                                                                                                              MICROGLOBULIN).
EMBL; X60693; G22868; PIR; J40540; J40540; HSSP; P03989; 14SAP.
PROSITE; PS00290; IG_MHC.
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STANDARD;
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HSSP; P01892; 1HHG.
MIM; 142800; -.
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                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE;
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DR PROSITE; PS00290; IG_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 24

HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT CHAIN 25 114 EXTRACELLULAR ALPHA-1.

FT DOWAIN 207 298 EXTRACELLULAR ALPHA-2.

FT DOWAIN 209 308 CONNECTING PEPTIDE.

FT DOWAIN 333 365 CYTOPLASMIC TAIL.

FT CARBOHYD 110 BY SIMILARITY.

FT DISULFID 277 288 BY SIMILARITY.

FT DISULFID 277 288 SY SIMILARITY.

FT DISULFID 277 288 SY SIMILARITY.

SQ SEQUENCE 365 AA; 40732 MM; BIC21094 CRC32;
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Query Match 50.0%; Score 77; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
Db 99 renlrialry 108
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earch completed. The Man

Search completed: Thu May 22 08:32:51 1997 Job time: 7 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:33:09 1997; MasPar time 3.22 Seconds 176.841 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-26 (1-20) from US08653294.pep 154 1 YRLAIRLNERRENLRIALRY 20 Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Database:

Mean 30.116; Variance 61.232; scale 0.492 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SOFTWARE	•	
Result No.	Score	Query Match	Length DB	DB	a	Description	Pred. No.
1	77	50.0	273	13	I38509	MHC class I histocom	5.918-01
c	77	0	27.4		T54463	ULA - 030	10-010
4 (				7 -	700	4	10.10
'n	`	50. O	Υ)	13	129308	н	5.91e-01
4	77	20.0	354	13	I80168	class I histocompati	5.91e-01
Ŋ	77	50.0	354	13	180167	class I histocompati	5.91e-01
Q	77	50.0		13	180171	н	5.91e-01
7	77	50.0		13	I80169	н	5.91e-01
80	77	50.0		7	HLHU12	las	5.91e-01
6	77	50.0		9	JH0539	class I histocompati	5.91e-01
10	77	50.0		9	B30345	MHC class I histocom	5.91e-01
11	77	50.0		13	I84486	transmembrane glycop	5.91e-01
12	77	50.0		ဖ	JH0540	class I histocompati	5.91e-01
13	77	50.0		9	S24434	class I histocompati	5.91e-01
14	77	50.0		9	A30345	MHC class I histocom	5.91e-01
15	77	50.0	362	13	137521	HLA-Bw57.2 antigen -	5.91e-01
16	77	50.0		13	159633	MHC HLA-B transmembr	5.91e-01
17	77	50.0		9	JH0541	class I histocompati	5.91e-01
18	77	50.0		13	I84490	lymphocyte antigen -	5.91e-01
19	77	50.0	362	13	162045	gene HLA B-1517 prot	5.91e-01
20	77	50.0	362	φ	A45834	lass I hist	5.91e-01
21	77	50.0	362	n	HLHUB8	MHC class I histocom	5.91e-01

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MCH class I HLA-B*51 class I histocompati MHC class I histocompati MHC class I histocompati MHC class I histocom HLA-AW24 protein - huma HLA-AW24 protein - huma HLC class I histocom MHC class I histocom MHC class I histocom M protein precursor M protein precursor Envotein precursor Con Intron 4 pittorin hotar 7 chai	beta-7 in gp12 in - hu
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ALIGNMENTS	DUIT 1 138509 #type fragment  RY MRC class I histocompatibility antigen - human (fragment)  ANISM #formal_name Homo sapiens #common_name man  06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change  06-Sep-1996  ESSIONS 138509  ERENCE Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.  #authors Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.  #authors Antigens (1994) 44:271-273  #title HLA-B*5105, a newly identified B51 IEF variant.	ule_ ues -ref Simi	74 renlrialry 83                        1               1
	RESULT 1 ENTRY TITLE TITLE DATE ACCESSIONS #authors #authors #title #title #cross-refe	NETI #no MMAR Quer Sest	Db 74 ren] Qy 11 RENI RESULT 2 ENTRY TITLE DATE ACCESSIONS REFERENCE # Journal # journal # title # cross-refe # accession

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I. #Journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897 #title A uniquely high level of recombination at the HLA-B locus. #cross-references WUID:94286544 #accession 159308
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**authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Warkins, D.I.

**journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897

**title A uniquely high level of recombination at the HLA-B locus.

**cross-references MUID:94286544
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##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05575; NID:9454767; CDS_PID:9454768
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##residues 1-354 ##label RES
##cross-references EMBL:U05579; NID:9454775; CDS_PID:9454776

XY #length 354 #checksum 5067
                                                              ##residues 1-274 ##label RES ##cross-references GB:M29864; NID:g187674; CDS_PID:g187675 Y #cross-references GB:M29864; NID:g187675 X
##molecule_type DNA ##residues 1-774 ##**:
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                                                                                                                                       Length 274;
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.

#journal Andly Acad. Sci. U.S.A. (1994) 91:5893-5897

# title A uniquely high level of recombination at the HLA-B locus. #cross-references WID:94286544

#accession 180171
                                                                                                                                                                          #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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                                                     #formal_name Pan paniscus #common_name pygmy chimpanzee,
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                                                                                                  24-May-1996 #sequence_revision 24-May-1996 #text_change
class I histocompatibility antigen - pygmy chimpanzee
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##cross-references EMBL:U05578; NID:9454773; CDS_PID:9454774
X #length 354 #checksum 3983
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##residues 1-355 ##label RES
##cross-references EMBL:U05582; NID:9454781; CDS_PID:9454782
XY #length 355 #checksum 6021
                                                                                                                                                                                                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 10; Conservative
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Best Local Similarity 100.0%;
Matches 10; Conservative
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220-285
SUMMARY
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115-206
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220-285
299-362
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25-362
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The seven exons correspond approximately to the domain structure of
this chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Malissen, M.; Malissen, B.; Jordan, B.R.
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
#title Exon/intron organization and complete nucleotide sequence of
    an HLA gene.
#cross-references MUID:82151002
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#product class I histocompatibility antigen HLA alpha
chain #status predicted #label MATN
#domain extracellular #status predicted #label EXTN
#domain alpha-1 #label EXIN
#domain alpha-2 #label EX2N
JH0539 #type complete
class I histocompatibility antigen Gogo-B0101 heavy chain
precursor - lowland gorilla
#formal_name Gorilla gorilla gorilla #common_name lowland
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#domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label INT\
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MHC class I histocompatibility antigen HLA alpha chain
precursor (clone pHLA 12.4) - human
#formal_name Homo sapiens #common_name man
05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996
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immunoglobulin homology
duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
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                                                                             ##cross_references EMBL:U05580; NID:9454777; CDS_PID:9454778
##cross_references EMBL:U05580; NID:9454777; CDS_PID:9454778
.X #length 355 #checksum 4603
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    #disulfide_bonds #status predicted
#length 359 #molecular-weight 40548 #checksum
                     ##molecule_type mRNA
##residues
| 3-366 ##7...
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 10; Conservative
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Best Local Similarity 100.0%;
Matches 10; Conservative
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#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HA-B51 and HIA-BW52 differ by only two amino acids which are in the helical region of the alpha-1 domain.
#cross-references WIDD:89080265
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#product class I histocompatibility antigen heavy chain,
Gogo-B0101 #status predicted #label CLA\
#domain alpha-1 #label AL1\
#domain alpha-2 #label AL2\
#domain alpha-3 #label AL3\
#domain immunoglobulin homology #label IMM\
#domain intracellular #label INT
#length 362 #molecular-weight 40170 #checksum 7327
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                                                                     #authors Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal J. Exp. Med. (1991) 1/4:1491-1509
#title Gorilla class I major histocompatibility complex alleles:
complactison to human and chimpanzee class I.
#accession JH0539
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MHC class I histocompatibility antigen HLA-Bw52 precursor
MLman
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30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 26-Apr-1996
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29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
26-Apr-1996
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#superfamily class I histocompatibility antigen;
immunoglobulin homology
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#checksum
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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#length 362 #molecular-weight 40521 #check
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Pred. No. 5.91e-01;
0; Mismatches 0
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##cross-references EMBL:X60255
##experimental_source EBV-transformed B cell
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Best Local Similarity 100.0%;
Matches 10; Conservative
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##residues 1-36
CLASSIFICATION #superfan
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11 RENLRIALRY 20

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RESULT

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99 renlrialry 108
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#authors
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SUMMARY
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#product class I histocompatibility antigen heavy chain,
Gogolo2 #status predicted #label CLA\
#domain alpha-1 #label ALI\
#domain alpha-2 #label ALI\
#domain alpha-2 #label ALS\
#domain inpha-3 #label ALS\
#domain intracellular #label INT\
#domain intracellular #label INT
#length 362 #molecular-weight 40204 #checksum 7312
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                                                                                                                       #authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.; Bias, W.B.; Parham, P. Bias, W.B.; Parham, P. Tissue Antigens (1994) 43:209-218
#title HiA-Bl5: Antigens (1994) 43:209-218
#cross-references MUID:94367483
#accession 184486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     class I histocompatibility antigen Gogo-B0102 heavy chain
precursor - lowland gorilla
#formal_name Gorilla gorilla gorilla #common_name lowland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P. #journal J. Exp. Med. (1991) 174:1491-1509 fritle Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I. #cross-references MUID:92078860
             transmembrane glycoprotein - human
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
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30-Jun-1992_#sequence_revision 30-Jun-1992 #text_change
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#length 362 #molecular-weight 40378 #checksum 9463
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                                                                                                                                                                                                                                                                                          ##rosidues 1-362 ##label RES
##cross-references GB:L15005; NID:g493154; CDS_PID:g493155
                                                                                                                                                                                                                            ##molecule_type mRNA
##residues
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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Pred. No. 5.91e-01;
0; Mismatches 0; Indels
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#type complete
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##residues 1-362 ##label LAW
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Best Local Similarity 100.0%;
Matches 10; Conservative
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99 renlrialry 108

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#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HIA-B51 and HIA-Bw52 differ by only two amino acids which are in the helical region of the alpha-1 domain.
#cross-references WUID:89080265
                                                                                                                                                                                                 Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; Mathins, H.F.; Troup, G.M.; Hughes, A.L.; Letvin, N.L. Nature (1922) 357:329-333

New recombinant Hia-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.
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E.H.
Gaps
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29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
06-Sep-1996
A30345; 168746
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##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #whenfamily class I histocompatibility antigen;
immunoglobulin homology
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#title Allelic variation in HLA-B and HLA-C sequences evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession 168746
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MHC class I histocompatibility antigen HLA-B51
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##residues 1-362 ##label HAY
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#accession S24434
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FITLE HA-Bw57.2 antigen - human ORGANISM #formal_name Homo saptens #common_name man formal_name Homo saptens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change O2-Jul-1996 Ptext_change O2-Jul-1996 Pte
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                                            #domain immunoglobulin homology #label IMM #length 362 #molecular-weight 40566 #checksum 9719
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Search completed: Thu May 22 08:33:25 1997 Job time : 16 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:33:42 1997; MasPar time 2.21 Seconds 98.639 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-26 (1-20) from US08653294.pep 154 Title: Description: Perfect Score:

1 YRLAIRLNERRENLRIALRY 20 Sequence:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 Database:

Mean 21.097; Variance 80.944; scale 0.261 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	-07	-07	-07	-07	90-	-02	-01	00+	00+	00+	00+	00+	00+	00+	00+	00+	00+	00+	
Pred.	1.21e-07	1.21e-07	6.09e-	6.09e-	3.05e-0	2.39e-05	9.02e-0	3.13e+0	3.13e+0(	3.13e+00	3.13e+00	3.13e+0(	3.13e+00	3.13e+00	3.13e+0	3.13e+0	3.13e+0(	3.13e+00	
Description	HLA-B2702 84-75-84 pa	CIL modu		_		HLA-B2702 84-75T/75-8	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	Alphal-helix of HLA-B	Peptide fragment of C	HLA-B2702 CTL modulat	HLAB38.6084.	HLA-B2702.60-84.	Peptide fragment of C	HLAB38 CTL modulating	Peptide fragment of H	HLA-B2702 CTL modulat	Sequence of HLA-Bw52	
£	R95428	R92907	R92909	R92908	R92910	R95430	R92911	R83062	R95413	R41208	R92912	R95422	R95416	R41205	R83093	R48286	R83090	R03142	
DB	18	16	16	16	16	18	16	16	18	ω	16	18	18	œ	16	ω	16	7	
Query Match Length DB	20	20	20	20	20	20	20	2	10	10	15	25	25	25	25	25	25	362	
Query Match	100.0	100.0	95.5	95.5	6.06	85.1	53.9	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	
Score	154	154	147	147	140	131	83	11	77	77	77	77	77	77	77	77	77	77	
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-B2702 C	HLA-B2702.75-84(D).	02.75-8	HLA-B2702 CTL modulat	702	HLA-B7.84-75-84 Palin	HLA-B7 CTL modulating	ACVS.	ACV synthetase.	SIVmac239 env gene pr	u	268-D.	EHV-4 gC.	Human L5/3 tumour sup	L5/3 tumour	3 tumour	Encoded by full-lengt	, E	Peptide fragment of C	HLA-B2705.75-84.	HLA-B2702 CTL modulat		HLA-B2702 CTL modulat	Sequence encoded by q	TrpE/androgen recepto
R83094	$\sim$	R95426	R83096	R83095	R95415	R92913	R40227	R13896	R24126	R21601	R38670	R20796	R66598	R66597	R66602	R66603	R44929	R41212	R95423	R83075	R95417		P70155	m
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## ALIGNMENTS

RESULT ID R AC R DT 1	LT 1 R95428 standard; peptide; 20 AA. R95428; 12-NOV-1996 (first entry)
KW	HLA-B2702 84-75-84 palindrome. HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate: membrane orderin: mammel; heat shock profein: Hsc70; apc
KK	s cell alcum, memorame process, mammas, med snow process, med, ore, ore, and salchum influx; cytotoxic T lymphocyte; CTL; differentiation;
SO	cycolysis; antigen presenting cell. Synthetic.
N C	WO9513288-A1.
7 F	10-NOV-1994; U12985.
PR	10-NOV-1993; US-150493.
P. P.	(STRD ) UNIV LELAND STANFORD JUNIOR. Clayberger C, Krensky AM:
DR	WPI; 95-194027/25.
ΡŢ	Compsns. comprising lymphoid surface membrane proteins - which may
PT	inhibit cytolytic activity and differentiation of CTLs.
ນ ເ	Example; Page 12; 29pp; English. R95413. and R95415-R95431 represent palindromes and fragments of
ខ	human-leucocyte-associated antidens. This sequence represents the
ပ္ပ	HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
ပ္ပ	the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
ပ္ပင္ပ	protein associated with T-cell activation in mammalian T-cells, and is
35	also immunologically cross reactive with the heat shock protein Asc/U.
88	expressed on B and T cells. p74 can be isolated by lysis of a suitable
ပ္ပ	cell with an amphoteric detergent, and then passed through an affinity
႘	column containing a covalently bound HIA-B2702 palindromic peptide.
ပ္ပင္ပ	Compositions comprising the extracellular fragment of p74 combined with HTA-B2702.60-84 (see R95416), induces calcium influx, and inhihits
ខ	cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
ပ္ပ	compounds can be screened for their effect on the cytolytic activity of
ပ္ပ	T-cells, by combining them with the extracellular portion of p74 and
ខ្ល	determining the amount of binding between the candidate compound and p74.
36	Modulation of the activity can be innibited in a celiular composition
ນບ	containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of b74. In an amount sufficient to compete
ខ	with p74 for the binding of the p74 ligand.
Ö	

Score 154; DB 18; Length 20; Pred. No. 1.21e-07; Query Match Best Local Similarity 100.0%; ö

Gaps

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
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HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherrapeutic amount of an immunosuppressant. This is administered the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTL, of the patient.
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                                                                                                                                                                                                                                                                                    Score 147; DB 16; Length 20; Pred. No. 6.09e-07; 0; Mismatches 1; Indels
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Pred. No. 6.09e-07;
0; Mismatches 1; Indels
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
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R92908 standard; peptide; 20 AA.
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R92910 standard; peptide; 20 AA.
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95.08;
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95.0%;
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Matches 19; Conservative
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12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
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12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                             20 AA;
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of a coeptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate for unhibit) the activity of the cytotoxic T lymphocytes (CTLS) of the patient.
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R83061-R83085, R83090-R83096 and R92907-R82913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of
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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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      Gaps
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HLA-B2702 CL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic T lymphocyte; CIL; major histocompatibility complex; MHC; firmunosuppressant; graft versus host disorder; transplantation; the class I MHC; HLA-B2702.
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   Indels
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   Mismatches
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(Clayberger C, Krensky AM, Parham P;
WPI; 95-358882/46.
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05-APR-1995, U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92907 standard; peptide; 20 AA.
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WPI; 95-358582/46.
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Indels

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Conservative

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Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

Example 20; 20pp; English.

This sequence represents the reservation of page 12; 20pp; English and the reservation of the res
                                                                                                                                                                              Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparated to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
12-O-1 1/2012 (first entry) (first entry)
13-O-1 1/2012 (first entry) (f
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                          Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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) UNIV LELAND STANFORD JUNIOR.
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Best Local Similarity
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WPI; 95-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the patient
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WO9513288-A1.
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STRD
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Score 131; DB 18; Length 20; Pred. No. 2.39e-05;

85.1%; 94.7%;

Best Local Similarity,

Query Match

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of
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    Gaps
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Pred. No. 9.02e-01;
  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krensky AM, Parham P;
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                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995.
05-ARR-1995.
05-ARR-1994; UG-22281.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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05-APR-1995.
05-APR-1994; UG-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R83062 standard; peptide; 10 AA.
                                                                                                                                                                       R92911 standard; peptide; 20
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                                            1 yrlairlnetrenlrialr 19
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Best Local Similarity 65.0%;
Matches 13; Conservative
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WPI; 95-358582/46.
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WPI; 95-358582/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
                                                                                                                                                                                                                                                                                                                                     Synthetic.
WO9526979-A1.
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WO9526979-A1.
                                                                                                                                                                                                                      16-MAY-1996
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11 RENLRIALRY 20
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WHY! 95-19402/125.

WHY! 95-19402/125.

WHY! 95-19402/125.

Thibit cytolytic activity and differentiation of CTLS.

Example; Page 11; 29pp; English.

This sequence represents the alphal-helix of the chunan-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cells, and is a look of the protein p74 from a T-cell lysate. p74 is a T-cells, and is a look of the protein associated with T-cell activation in mammalian T-cells, and is a look of the protein associated with T-cell solutive with the heat shock protein HSC70.

Expressed on B and T cells. p74 can be isolated by lysis of a suitable compositions comperising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing the binding of the p74 in an amount sufficient to compete containing the mach and p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient to compete the p74 in an amount sufficient to compete containing the protein p74 in an amount sufficient protein protein protein protein protein protein protein protein
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Alphal-helix of HLA-B2702.
Alphal-helix, alphal-helix, human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of mine (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
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                                                                                                                                                                                                                                                       Score 77; DB 16; Length 10; Pred. No. 3.13e+00;
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Pred. No. 3.13e+00;
0; Mismatches 0:
                                                                                                                                                                                                                                                                                                              0; Mismatches
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytolysis; antigen presenting cell.
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R95413 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                           Best Local Similarity 100.0%;
Matches 10: Concern
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Best Local Similarity 100.0%;
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11 RENLRIALRY 20
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70.84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
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HLA-B2702 CTL modulating peptide (B2702.70-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                               New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 11; Page 54; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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Pred. No. 3.13e+00;
0; Mismatches 0;
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                                                                                                                                                                                                      25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clarberger CA, Frensky AM;
WPI; 93-303134/38.
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05-APR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
CLAYDETGET C, KTENSKY AM, PATHAM F
WPI; 95-338582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 11
R92912 standard; peptide; 15 AA.
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Matches 10: Consequent
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and R95415-R95431 represent palindromes and fragments of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the company of the control of control 
                                                                                                                                                                                             HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; real lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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HIA-B2702-50-84.
HIA-B2702-50-84.
HIA-P3707-19 alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
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Pred. No. 3.13e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD) UNIV. LELAND STANFORD JUNIOR.
CLAYDETGER C, KIENSKY AM;
WPI; 95-194027/25.
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDerger C, Krensky AM;
WPI; 95-194027/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R95416 standard; peptide; 25 AA.
R95416;
                                                                              R95422 standard; peptide; 25 AA.
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Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                       12-NOV-1996 (first entry)
HLAB38.6084.
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                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1995.
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                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                               R95422;
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                                                      RESULT
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Name of the control o
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WPI; 93-301134/38
New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 8; Page 53; 61pp; English.
The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL coxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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14205 standard; peptide; 25 AA.
R41205;
R41205;
15-MAR-1994 (first entry)
15-MAR-1994 (first entry)
Hupan leukocyte antigen; HLA, peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
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Pred. No. 3.13e+00;
0; Mismatches 0; Indels
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Pred. No. 3.13e+00;
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HLAB38 CTL modulating peptide (B38.6084).
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25-FEB-1993. 001758.
02-MAR-1992. UG-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 15
R83093 standard; peptide; 25 AA.
R83093;
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Local Similarity 100.0%;
Les 10; Conservative
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Best Local Similarity 100.0%;
Matches 10; Conservative
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Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of Colass I major histocompatibility complex (MRC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLAB38.
Synthetic.
WQ9526979-A1.
                                                                                                               12-OCT-1995.
05-APR-1995, U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Gaps ö Score 77; DB 16; Length 25; Pred. No. 3.13e+00; 0; Mismatches 0; Indels Ouery Match 50.0%; Best Local Similarity 100.0%; Matches 10; Conservative

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16 renlrialry 25 |||||||||||||| |11 RENLRIALRY 20

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Search completed: Thu May 22 08:33:50 1997 Job time: 8 secs.

1.74e+01 1.74e+01 2.58e+01 2.58e+01 2.58e+01 2.58e+01 2.58e+01 2.58e+01 2.58e+01 3.79e+01 
1 1880 8 RPAL_SULAC 1 1748 7 POLR_ELV 1 334 1 BIOB_BREFL 1 347 10 VALL_ELCV 454 1 ACH5_CHICK 1 508 7 PGKD_TRYBB 1 527 6 MERA_TRADI 622 1 ACH4_CHICK 1 529 6 MERA_TRADI 1 289 6 MSH_TREST 1 1281 6 MDR3_CRIGK 1 1898 10 VGNB_CPSMY	53 54.1 3391 7 POLG_DEN27 GENOME POLYPROTEIN (C 53 54.1 3391 7 POLG_DEN26 GENOME POLYPROTEIN (C 52 53.1 122 8 RL17_CHLTR 50S RIBOSOMAL PROTEIN 52 53.1 1611 YD95_YEAST HYPOTHETICAL 18.9 KD 57 53.1 367.1 1849 HTMAN HIA CLASS	52 53.1 362 1 1B62_HUMAN HLA CLASS I HISTOCOMP	52 53.1 36.2 1 1B5.2 HUMAN HLA CLASS I HIGTOCOMP 52 53.1 47.3 1 BGLB_MICBI THERMOSTABLE BETA-GLU 52 53.1 609 7 PRXC_CURIN VANADIUM CHLOROPEROXI 52 53.1 68.2 7 PRC_ECOLI TAIL-SPECIFIC PROTEAS	52. 53.1 948 7 PMA3_ARATH PLASMA MEMBRANE ATPAS ALIGNMENTS	RESULT 1 . ID STANDARD; PRT; 375 AA.		01-NOV-1995 (REL. 32, LAST HRWA PROTEIN. HRWA.		SEQUENCE FROM N.A. STRAIN-PSS61;	RA HUANG H.C., HUTCHESON S.W., COLLMER A.; RL MOL. PLANT MICROBE INTERACT. 4:469-476(1991). RN [2] RP SEQUENCE FROM N.A.	RC STRAIN-PSS61; RX MEDILINE; 94100578. RA HEU S., HUTCHESON S.W.; RL MOL. PLANT MICROBE INTERACT. 6:553-564(1993). CC -!- FUNCTION: UNKNOWN. MAY SERVE A REGULATORY FUNCTION.	DR EMEL: 114926; G294367;  KW HYPERSENSITIVE RESPONSE.  SQ SEQUENCE 375 AA; 41458 MW; 733EEB06 CRC32;  Query Match 64.3%; Score 63; DB 5; Length 375;  Best Local Similarity 58.3%; Pred. No. 4.00e-01;  Matches 7; Conservative 2; Mismatches 3; Indels 0; Gal	Db 174 yrlsitrktlsy 185    :   :     Qy 1 YRLAIRRIARY 12	50	DT 01-MAR-1989 (REL. 10, CREATED) DT 01-ANG-1992 (REL. 23, LAST SEQUENCE UPDATE) DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE) DE STREPTOMYCIN BIOSYWHESIS PROTEIN STRE.	STRF. STREPTOMYCES PROKARYOTA;
**************************************	Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.	MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Run on: Thu May 22 08:35:52 1997; MasPar time 2.11 Seconds 120.401 Million cell updates/sec Tabular output not generated.	>US-08-653-294- on: (1-12) from USC core: 98	Sequence: 1 YRLAIRRIALRY 12 Scoring table: PAM 150 Gap 15	Searched: 59021 seqs, 21210388 residues	Post-processing: Minimum Match 0% Listing first 45 summaries	Database: swiss-prot34	Statistics: Mean 28.088; Variance 37.415; scale 0.751	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES  Result Query  No. Score Match Length DB ID Description Pred. No.	HEMA PROTEIN. STREPTOMYCIN BIOSYMTH HIA CLASS I HISTOCOMP PROBABLE BETA GLUCOSI NEURONAL ACETYLCHOLIN NEURONAL ACETYLCHOLIN	56 57.1 499 1 ACH3 KAT NEURONAL ACETYLCHOLIN 56 57.1 502 1 ACH3 HUMAN NEURONAL ACETYLCHOLIN 56 57.1 1151 4 GRRI_YEAST GRRI PROTEIN. 55 56.1 212 11 YCD4_YEAST HYPOTHETICAL 23.6 KD 55 56.1 401 1 ACH4 YEAST ACHATICAL 23.6 KD	55 56.1 493 1 ACHE_HUMAN ACETYLCHOLINE RECEPTO 55 56.1 583 9 RUBZ_BRANA RUBISCO SUBUNIT BINDI 55 56.1 844 3 DILAG-HUMAN DNA LIGASE IV (EC 6.5 55 56.1 1420 1 APOA MACMU APOLIPOPROTEIN(A) (EC	54 55.1 298 9 RT03_ACACA MITOCHONDRIAL RIBOSOM 35 5.1 493 1 ACHE_MOUSE ACETYLCHOLINE RECEPTO 54 55.1 494 1 ACHE_RAT ACETYLCHOLINE RECEPTO 54 55.1 500 1 ACH4_DROME ACETYLCHOLINE RECEPTO	54 55.1 651 11 YHJK_ECOLI HYPOTHETICAL 73.1 KD 1 54 55.1 699 8 PTGA_BACSU PTS SYSTEM, GLUCOSE-S 1 54 55.1 850 8 RN12_YEAST RNA12 PROTEIN.

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Gaps

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REPUBLICE OF 461-477 FROM N.A.

RA VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;

RA VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;

J. BACTERIOL. 170:3703-3710(1988).

C. :- CATALYIT ACTIVITY: HURDOLYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.

C. :- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.

DR EMBL; D30/62; G10632; -: NOT_ANNOTATED_CDS.

BREI: M216/2: -: NOT_ANNOTATED_CDS.

DR SUBTILIST; BG11181; YCKE.

DR SUBTILIST; BG10633; GLYCOSYL, HYDROL_F1_1.

DR ROSITE; PS00673; GLYCOSYL, HYDROL_F1_2.

RW HYPOTHETICAL PROTEIN; HYDROLASE; GLYCOSIDASE; CELLULOSE DEGRADATION.

FT ACT_SITE 170 170 PROTON DONOR (POTENTIAL).

FT ACT_SITE 378 NUCLEOPHILE (BY SIMILARITY).

FT FOTHER STATE 378 NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                          BACILLUS SUBTILIS.
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE.
-:- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; X57032; G297763; --
PROSITE: PS00236; NEUROTR. ION_CHANNEL.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; SIGNAL;
STRANSEMBRANE; MULICENE FAMILY.
SIGNAL.
1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92319195.
CRIADO M., ALAMO L., NAVARRO A.;
NEUROCHEM. RES. 17:281-287(1993).
-!- FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBJUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                      01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
1-EEB-1996 (REL. 33, LAST ANOTATION UPDATE)
PROBABLE BETA-GLUCOSIDASE (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)
(BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGDALASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
SEVENTINE, (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VENTEBRATA; TETRAPODA; MANMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 1; Length 477; Pred. No. 5.20e+00; 4; Mismatches 1; Indels
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                  477 AA
                    PRT;
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MICROBIOLOGY 141:277-279(1995).
                                                       CREATED)
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ilarity 54.5%;
Conservative
                    STANDARD;
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2 RLAIRRIALRY 12
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   MEDLINE; 95219080
LT: 4
BGLZ_BACSU
P42403;
01-NOV-1995 (
01-NOV-1995 (
01-NOV-1995 (
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ACH3_BOVIN
Q07263;
01-7
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Matches
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HARA CLASS I HISTOCOMPATIBLILTY ANTIGEN, F ALPHA CHAIN PRECURSOR (HLA ANTIGEN) (LEUKOCYTE ANTIGEN F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.

EXTRACELULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                       Gaps
                          MEDLINE; 91375432.

A MEDLINE; 91375432.

A MANSOURI K., PIEPERSBERG W.;
L MOLL GEN. CENET. 228.459-469(1991).

C -1 FUNCTION: MAY BE INVOLVED IN THE FORMATION OF N-METHYL-L-GLUCOSAMINE.

C -1 PATHWAY: STREPTOMYCIN BIOSYNTHESIS.

C -1 SIMILARITY: LOW, TO THE AMINO-TERMINAL DOMAIN OF GLUCOSE-6-BOSPHATE ISOMERASE.

R PHEL; YOLGS9; EILHJ12; ALT_RINT.

R PREL; YOLGS9; EILHJ12; ALT_RINT.

R PREL; YOLGS9; EILHJ2; ALT_RINT.

R PRE; S17776; S17776.

STREPTOMYCIN BIOSYNTHESIS.

STREPTOMYCIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE, 93246295.
OTTING N., BONTROR R.E.;
IMMUNOSENETICS 38:141.145(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MACACA MULATTA (RHESUS MACAQUE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; Z1819; G38569; -.
PIR; S29990; S29990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 5; Length 348; Pred. No. 5.20e+00; 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                Length 281;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                Score 57; DB 9; Len
Pred. No. 5.20e+00;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
3A375142 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 P
39300 MW;
                                                                                                                                                                                                                                                                58.2%;
ilarity 70.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P03989; 1HSA;
PROSITE; PS00290; IG_MHC
MHC I; TRANSMEMBRANE; GL
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 rvalrkillry 108
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226
109
348 AA;
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2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                         234 rlaarrlamr 243
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Best Local Similarity
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Matches 6; Conser
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 SEQUENCE FROM N.A.
                    STRAIN=N2-3-11;
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DOMAIN
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DISULFID
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SEQUENCE
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Gaps

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7
ACH3_RAT
P04757:
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SEQUENCE
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                                                                            Matches
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    SELE
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                                                                                                                                                                                                                                                                                            GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
        EXTRACELLORAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (BY SIMILARITY).
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND THREE NON-ALPHA CHAINS.
-: DEVELOPMENTAL STAGE: HIGH LEVELS IN THE DEVELOPING CILIARY AND SUPERIOR CERVICAL GANGLIA.
-: SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN.
-: SUMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                     01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE; 91009210.
COUTURIER S., ERMANN L., VALERA S., RUNGGER D., BERTRAND S.,
BOULTER J., BALLIVET M., BERTRAND D.;
J. BIOL. CHEM. 265:17560-17567(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X07345; G211045; -
EMBL; X07345; G211045; -
EMBL; X07345; G871036; -
EMBL; X07346; G871036; JOINED.
EMBL; X07347; G871036; JOINED.
PIR; S00378; ACCH3N.
PROSITE; PS00236; NEUROTR_ION_CHANNEL.
PROSITE; PS00236; NEUROTR_ION_C CHANNEL.
TRANSMEMBRANE; MULTIGENE FAMILY.
SIGNAL.
23 496 ACETYLCHOLINE RECEPTOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88283624.
NEF P., ONEYSER C., ALLIOD C., COUTURIER S., BALLIVET M.; EMBO J. 7:595-601(1988).
                                                                                                                                    Score 56; DB 1; Length 495; Pred. No. 7.83e+00; 2; Mismatches 3; Indels
                                                                                                          POTENTIAL.
63BE4C2E CRC32;
                                                                                                                                                                                                                                     496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC.
                                                                                                 POTENTIAL.
                                                                                                                   MM:
                                                                                                                                                                                                                                                                                                                                                                                [2] SEQUENCE OF 81-496 FROM N.A. MEDLINE; 88283624.
                                                                                                                                     57.1%;
Similarity 58.3%;
7: Conservative
                                                                                                                   56914
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                          223 yslyirrlplfy 234
                                                                                                                                                                                             1 YRLAIRRIALRY 12
                                                                                              45
162
195 AA;
                                                                                                                                     Query Match
Best Local Similarity
Matches 7: Conser
 22
231
2531
2563
2563
319
468
149
                                                                                                                                                                                                                                                                                                                 GALLIFORMES.
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АСНЗ_СНІСК
P09481;
CHAIN
DOMAIN
TRANSMEM
TRANSMEM
TRANSMEM
                                                DOMAIN
TRANSMEM
DISULFID
DISULFID
                                                                                                         CARBOHYD
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TRANSMEM
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TRANSMEM
DISULFID
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELLULAR: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; X03440; G758258; --
EMBL; X03440; G758258; --
EMBL; L31621; G468916; --
EMBL; L04951; G484069; --
PIR; A24572; A24572.
PIR; A24572; A24572.
TRANSMENBRANE; DONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
TRANSMENBRANE; MULTIGENE FAMILY.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A.
MEDLINE; 86118671.
BOULTER J., EVANS K., GOLDMAN D., MARTIN G., TRECO D., HEINEMANN S.,
PATRICK J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 88041184.
BOULTER J., CONNOLLY J., DENERIS E.S., GOLDMAN D.J., HEINEMANN S.F.,
PATRICK J.;
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 94193711.
YANG X., MCDONOUGH J., FYODOROV D., MORRIS M., WANG F.,
DENERLS E.S.,
DENERLS E.S.,
1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS IO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBERANE.
ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                               ö
                                                                                                                                  Length 496;
                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROC. NATL. ACAD. SCI. U.S.A. 84:7763-7767(1987)
                                                                                                                                Score 56; DB 1; L
Pred. No. 7.83e+00;
2; Mismatches 3
                                                                                        883D3EA9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC.
                                                                      PROBABLE
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                           MM;
                                                                                                                                57.1%;
58.3%;
                                                                 163 57027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-21 FROM N.A. TISSUE-LIVER;
                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 319:368-374(1986).
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2334 259 259 259 322 322 471 167 218 218
                                                                                                                                                                                                                           224 yslyirrlplfy 235
                                                                                                                                                                                                                                                                     1 YRLAIRRIALRY 12
                                          46
163
496 AA;
                                                                                                                                     Query Match
Best Local Similarity
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386 yrlmikrinfsf 397
CONFLICT
                 SEQUENCE
                                    Query Match
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REPEAT
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REPEAT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00236; NEUROTR_ION_CHANNEL.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
TRANSMEMBRANE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3. EXTRACELLULAR.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                ANAND R., LINDSTROM J.;
SUBMITTED (JUN-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
-!- SUBCELDULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; M55239; G35090; -.
EMBL; M55239; G35090; -.
EMBL; M5559; G34986; -.
PIR; A37040; A33040.
PIR; S24595; S24595.
                                                                                                                                  01-OCT-1993 (REL. 27, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
VSLPLACRA -> ALAAPGAVAP (IN REF. 2).
D -> G (IN REF. 1).
DD -> TT (IN REF. 1).
                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                           ö
                         Score 56; DB 1; Length 499;
Pred. No. 7.83e+00;
                                           3; Indels
                                                                                                                                                                                                                                  FORNASARI D., CHINI B., TARRONI P., CLEMENTI F., NEUROSCI. LETT. 111:351-356(1990).
166 PROBABLE.
56997 MW; E561713C CRC32;
                                           2; Mismatches
                                                                                                                  502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                    TISSUE-THYMUS;
MEDILUS; 91114756.
MIHOVILOYIC M., ROSES A.D.;
EXP. NEUROL. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 29-502 FROM N.A.
                         57.1%;
58.3%;
                                            7; Conservative
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
169
13
99
                                                            227 yslyirrlplfy 238
                                                                             1 YRLAIRRIALRY 12
166 1
499 AA;
                                   Best Local Similarity
                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 90245296.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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169
5
99
131
                                                                                                                                                                                                                                                                                                                                                                              MEMBRANE.
                                                                                                                                                                                                                                                                                                                          LISSUE-BRAIN;
                                                                                                 8
ACH3_HUMAN
P32297;
01-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 118503;
CARBOHYD
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CONFLICT
CONFLICT
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TRANSMEM
                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 4; Length 1151;
Pred. No. 7.83e+00;
4; Mismatches 3; Indels
                                            Score 56; DB 1; Length 502; Pred. No. 7.83e+00;
                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASN-RICH.
LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8C0DEF89 CRC32;
I -> S (IN REF. 1)
L -> V (IN REF. 1)
75D79DEC CRC32;
                                                                                                                                                                                                                              GRRI OR COTZ OR CATBO OR YJR090C OR JJ885.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTINA, HEMIASCOMYCETES.
                                                                                                                                                                                01-WAR-1992 (REL. 21, CREATED)
01-WAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                    2; Mismatches
                                                                                                                                                             PRT; 1151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUCINE-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ASN
                                                                                                                                                                                                                                                                                                   FLICK J.S., JOHNSTON M.;
MOL. CELL. BIOL. 11:5101-5112(1991).
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LERR
LERR
LERR
LERR
LERR
                      57245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCOSE METABOLISM; REPEAT;
DOMAIN 38 49
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                                             / Match 57.1%;
Local Similarity 58.3%;
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similarity 41.7%;
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MEDLINE; 96437976.
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SEQUENCE FROM N.A.
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GRR1_YEAST
P24814;
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22 42 85.7 938 14 B30 24 42 85.7 1536 4 A30 25 42 85.7 1536 4 A30 26 42 85.7 1536 4 R32 28 41 83.7 359 9 A48 29 41 83.7 360 16 A48 31 41 83.7 360 7 532 33 41 83.7 360 7 532 34 41 83.7 360 7 532 35 41 83.7 360 7 532 36 41 83.7 360 7 532 37 41 83.7 360 7 532 38 41 83.7 360 7 532 39 41 83.7 360 7 532 39 41 83.7 360 7 532 39 41 83.7 732 13 JC4 42 41 83.7 732 13 JC4 43 41 83.7 732 13 JC4 44 41 83.7 783 1 JUD6 45 41 83.7 783 1 JUD6 45 41 83.7 783 1 JUD6 45 41 83.7 783 1 JUD6 46 41 83.7 783 1 JUD6 47 41 83.7 783 1 JUD6 48 41 83.7 783 1 JUD6 49 41 83.7 783 1 JUD6 40 41 83.7 783 1 JUD6 41 83.7 783 1 JUD6 42 41 83.7 783 1 JUD6 43 41 83.7 783 1 JUD6 44 41 83.7 783 1 JUD6 45 51593 #EQUER 46 FERENCE 45 HOLDACTERIUM PARALLICLE 46 FILLE 47 HOLDACTERIUM PARALLICLE 48 FILLE 51593 51593 51593 51593 51593 51593 51593 51593 51593 51593 51593	##TCSS.references EMBL:X5443 SUMMARY  Query Match  Best Local Similarity 83.3%; Sco Best Local Similarity 83.3%; Pro Matches 5; Conservative 1  Db 154 yrlavr 159    1   :   Conservative 1   YRLAIR 6
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						н	RESULT
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1.02e+02	protein-tyrosine-pho	S12050	φ	1997	83.7	41	45
.02e+		JDEC22	-	7	83.7	41	44
9	DNA-directed DNA pol	S19263	Ŋ	9	m	41	43
1.02e+02	1-per	55	13	m	83.7	41	42
	acylaminoacyl-peptid	52	Н	m	3	41	41
1.02e+02	DNA-directed DNA pol	S34120	16	$^{\circ}$	m	41	40
•		S17671	9	æ	3	41	39
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1.02e+02	photosystem ii piote	717469		ט כ	3 (	† <del>-</del>	י מ
1.02e+02	H	B25362	۱ م	360	283	7.	<b>†</b> 1
	photosystem II prote	S54256	7	9	ന	41	33
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	н	S26586	7	9	e,	41	31
1.02e+02	റ	S45009	7	9	ന	41	30
•	Н	A48306	16	9	83.7	41	29
٠	photosystem II prote	F2MWD1	4	S	m	41	28
	nitrogen requlatory	S53023	7	4	3	41	27
ø.	cular-weig	A48654	σ	93	'n.	42	56
φ.	U	A33988	11	σ	S	42	25
φ.	otein	RGBYS3	4	53	S	42	24
6.68e+01	alpha-adaptin A - mo	A30111	14	~	85.7	42	23
φ.	alpha-adaptin C - mo	B30111	14	m	S	42	22

S15593 #type complete hypothetical protein (insertion sequence ISH27-3) - Halcharterium balckium	######################################	\$15593 \$15591 Pfelfer, F.; Blaseio, U. Nucleic Acids Res. (1990) 18:6921-6925 Transposition burst of the ISH27 insertion element family in Halobacterium halobium.	sl sl fer #1	similarity 83.3%; Score 47; DB 16; Length 388; Similarity 83.3%; Pred. No. 7.12e+00; 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	/r 159 :  IR 6	D49898 #type complete cellobiose phosphotransferase system celC - Bacillus stearothermophilus #formal_name Bacillus stearothermophilus 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 A49898 A49898 Lai, X.; Ingram, L.O. J. Bacteriol. (1993) 175:6441-6450 Cloning and sequencing of a cellobiose phosphotransferase system operon from Bacillus stearothermophilus XL-65-6 and functional expression in Escherichia coli.
RESULT 1 ENTRY TITLE	ORGANISM DATE	ACCESSIONS REFERENCE #authors #journal #title	#cross-refere #accession #statucs ##residues ##residues ##cross-re	Query Match Best Local Si Matches	Db 154 yrlavr           Qy    YRLAIR	ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE # authors # fournal # title

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- fission yeast (Schizosaccharomyces
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Gene (1993) 131:135-139
Sequence analysis of closely related retrotransposon families
from fission yeast.
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#formal_name Schizosaccharomyces pombe
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28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change
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#length 1333 #molecular-weight 154915 #checksum 3353
                                              #residues 1-245 ##label LAI
#cross-references NCBIN:138630; NCBIP:138634
#note sequence extracted from NCBI backbone
#length 245 #molecular-weight 27430 #checksum 647
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Pred. No. 1.13e+01;
1; Mismatches 0; Indels
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Mol. Cell. Biol. (1990) 10:6791-6798
Two related families of retrotransposons from
                                                                                                                                     Score 46; DB 10; Length 245;
Pred. No. 1.13e+01;
1; Mismatches 0; Indels
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1; Mismatches 0; Indels
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*cross-references MUID:91061791
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hypothetical protein Tfl -
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              ##status preliminary
##molecule_type DNA
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##CCESSION A43015
##Rocession A43015
##residues 1-1132 ##label SAN
##residues 1-1132 ##label SAN
##residues 1-1132 ##label SAN
##residues 1-1132 ##label SAN
Gene J protein makes up the distal fiber of the phage tail. It is
responsible for adsorption to the host during infection and
determines host specificity. It specifically binds to the lambda
receptor protein of E. coil file. This receptor protein encoded by
E. coll gene lamb is an outer membrane protein that functions in
the transport of maltose and maltodextrins.

DAMENT Under the action of the gene G, T, H, M, L, K, and I proteins, gene
J protein serves as the initiator of tail polymerization. There
are 2-4 copies of protein J per mature phage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD / U96 #type complete nudel protein precursor - fruit fly (Drosophila melanogaster) #formal_name Drosophila melanogaster 27-oct-1995 #sequence_revision 27-oct-1995 #text_change AS7096 AS7096
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the nudel gene, is involved in defining embryonic
dorsoventral polarity in Drosophila.
A57096
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                                                                                                                                                                                                                                                                                                                                                                              submitted to the Nucleic Acid Sequence Database, September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily LDL receptor ligand-binding repeat homology extracellular protein
                                          OSBPL #type complete host specificity protein J - phage lambda #formal_name phage lambda 13.Jun-1983 #text_change
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CLASSIFICATION #superfamily phage lambda host specificity protein J
SUMMARY #length 1132 #molecular-weight 124421 #checksum 1868
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#title Nucleotide sequence of bacteriophage lambda DNA.
#cross-references MUID:83189071
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2; Mismatches 0; Indels
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Cell (1995) 82:785-794
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Best Local Similarity 66.7%;
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Trypanosoma cruzi
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                            #domain LDL receptor ligand-binding repeat homology #label LDL3 #molecular-weight 292372 #checksum 9962
#domain LDL receptor ligand-binding repeat homology
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hypothetical protein DGF-1 - Trypanosoma cruzi
#formal_name Trypanosoma cruzi
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
03-Mar-1995
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##note sequence extracted from NCBI backbone
XX #hote #length 3229 #molecular-weight 334929 #checksum
                                                                                                                                                                                                                                                                                                                                     Wincker, P.; Murta-Dovales, A.C.; Goldenberg, S. submitted to the EMBL Data Library, April 1992 Nucleotide sequence of a representative member of Trypanosoma cruzi dispersed gene family.
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#journal Mol. Blochem. Parasitol. (1992) 55:217-220
#title Nucleotide sequence of a representative member of Trypanosoma cruzi dispersed gene family.
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Pred. No. 1.78e+01;
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Matches 5; Conservative
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S31175 #type complete
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Gene (1992) 122:381-382
Cloning of a cDNA encoding the Tcp-1 (t complex polypeptide 1) homologue of Arabidopsis thaliana.
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##residues
1-772 ##label MAR
##cross-references DDBJ:D78001

This enzyme belongs to alpha-amylase family. It catalyzes the
conversation of maltodextrins to maltocligosyl trehaloses by
forming alpha,alpha-1,1-glucosidic linkage by an intramolecular
transglucosylation.
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JNO448 #type complete
t-complex polypeptide Tcp-1 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993 JN0448
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alpha.alpha-trehalose-phosphate synthase (EC 2.4.1.-) -
Rhizobium sp.
#formal_name Rhizobium sp.
10-May-1996 #sequence_revision 19-Jul-1996 #text_change
19-Jul-1996
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30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Sep-1993
831175
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##cross-references DDBJ:D11351
X #length 545 #molecular-weight 59229 #checksum 1573
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#length 772 #molecular-weight 84859 #checksum
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Pred. No. 2.79e+01;
1; Mismatches 0; Indels
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Yeast ribosomal protein Li is required for the stability of newly synthesized 55 rRNA and the assembly of 605 ribosomal subunits.
                Blinov, A.G.; Sobanov, Y.V.; Bogachev, S.S.; Donchenko, A.P.;
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#authors Tang, B.; Nazar, R.N.
#journal J. Blol. Chem. (1991) 266:6120-6123
#title Structure of the yeast ribosomal 5 S RNA-binding protein YL3
#accession S14172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang, B.; Nazar, R.N. J. Biol. Chem. (1992) 267:17738-17742 Unbalanced regulation of the ribosomal 5 S RNA-binding protein in Saccharomyces cerevisiae expressing mutant 5
                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein L5.e - yeast (Saccharomyces cerevisiae) protein LPI14w; protein YPL131w; ribosomal protein YL1; ribosomal protein YL3
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03-May-1994 #sequence_revision 27-Jan-1995 #text_change
06-Sep-1996
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The 5-S RNA binding protein from yeast (Saccharomyces cerevislae) ribosomes. Evolution of the eukaryotic?
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                               Filippova, M.A.
Mol. Gen. Genet. (1993) 237:412-420
The Chironomus thummi genome contains a non-LTR
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**NCE S11574
**Loss-references EMBL:M94864
**Loss-references EMBL:M94864
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##note the nucleotide sequence wa
Library, September 1992
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#cross-references MUID:80112896
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ilarity 83.3%;
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2-31,209-256 ##label NAZ
the sequence from the summary and Fig. 5 is inconsistent
with that from tables 2 and 3 in having 17-Tyr
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arow protein - Emericella nidulans
blosynthetic dehydroquinase
3-dehydroquinate dehydratase (EC 4.2.1.10); 3-dehydroquinate
synthase (EC 4.6.1.3); 3-phosphoshikimate
1-carboxyvinyltransferase (EC 2.5.1.19); shikimate
5-dehydrogenase (EC 1.11.25); shikimate
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                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1995
The sequence of Saccharomyces cerevisiae chromosome XVI left
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                                                                               S69040
Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.;
Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wang, Y.; Winnett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Charles, I.G.; Keyte, J.W.; Brammar, W.J.; Smith, M.;
Hawkins, A.R.
#journal Nucleic Acids Res. (1986) 14:2201-2213
#title The isolation and nucleotide sequence of the complex AROM
#cross-references wIUD:86176723
#accession A24962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #product ribosomal protein L5.e #status experimental
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31.Mar-1990 #sequence_revision 31-Mar-1990 #text_change
18-Aug-1995
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##label CHA
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Pred. No. 4.33e+01;
1; Mismatches 1; Indels
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##molecule_type DNA
1-1603 ##label DUN
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##residues 1-297 ##label HAL
##cross-references EMBL:U43703
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#accession A24042
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CLASSIFICATION #sup
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Pappu, H.R.; Karasev, A.V.; Anderson, E.J.; Pappu, S.S.; Hilf, M.E.; Febres, V.J.; Eckloff, R.M.; McCaffery, M.; Boyko, V.; Gowda, S.; Dolia, V.V.; Koonin, E.V.; Gumpf, D.J.; Cline, K.C.; Garnsey, S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.
Virology (1994) 199:35-46
Nucleotide sequence and organization of eight 3' open reading
aromatic amino acid biosynthesis; ATP binding; carbon-oxygen lyase; hydro-lyase; multifunctional enzyme; NADP; oxidoreductase; phosphorus-oxygen lyase; phosphotransferase; transferase
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annotation; erratum; corrections to coding regions
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                                                                                                     #domain 3-dehydroquinate synthase homology #label DQS/
#domain 3-phosphoshikimate 1-carboxyvinyltransferase
homology #label PSR/
#domain shikimate kinase homology #label SKI/
#domain shikimate kinase homology #label SKI/
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25. CP-capsid protein - cirrus tristeza closterovirus CTV #common name cirrus tristeza closterovirus CTV #common name cirrus tristeza closterovirus CTV 11-oct-1994 #sequence_revision 11-oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, #journal Virology (1986) 151:350-361
#title Cloning and Sequencing of the genetic right end of bacterlophage T3 DNA.
#cross-references MUID:86209997
                                                                                                                                                                                                                                #domain shikimate dehydrogenase homology #label SKD #length 1603 #molecular-weight 175079 #checksum 7102
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gene 18.7 protein - phage T3
#formal_name phage T3
host Escherichia coli
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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##residues 1-83 ##label YAM
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	utp on:	able: PA	59021 seqs, 21	Post-processing: Minimum Match 0% Listing first 45 summaries	Database: swiss-prot34 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11	Statistics: Mean 23.812; Variance 26.364; scale 0.903	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	8 Result Query No. Score Match Length DB ID Description Pred. No.	1 48 90.6 832 11 YCZ6_YEAST PUTATIVE 95.7 KD TRAN 5.28e+00 3 47 88.7 142 10 VPRL_MOUSE IMMUNOGLOBULIN IOTA C 8.51e+00 5 47 88.7 142 10 VPRL_MOUSE IMMUNOGLOBULIN IOTA C 8.61e+00 6 47 88.7 142 10 VPRL_MOUSE IMMUNOGLOBULIN IOTA C 8.61e+00 6 47 88.7 225 2 CABIO_SALIY COBALT TRANSPORT PROT 8 6.1e+00 6 47 88.7 49.6 6 MMSA_PSEAE METHYLMALONATE-SEMIAL 8.61e+00 8 46 86.8 3.28 4 HALQ_MOUSE H-2 CLASS I HISTOCOMP 1.39e+01 10 46 86.8 346 7 PILZ_TRYBB SERINE_YTHEONINE PROT 1 39e+01 11 46 86.8 346 7 PILZ_TRYBB SERINE_YTHEONINE PROT 1 39e+01 11 46 86.8 346 7 PILZ_TRYBB SERINE_YTHEONINE PROT 1 39e+01	46 86.8 362 4 HA13 MOUSE H-2 CLASS I HISTOCOMP 46 86.8 362 1 1B18_HUMAN HLA CLASS I HISTOCOMP 46 86.8 362 1 1B18_HUMAN HLA CLASS I HISTOCOMP 46 86.8 362 1 1B16_HUMAN HLA CLASS I HISTOCOMP 46 86.8 362 1 1B19_HUMAN HLA CLASS I HISTOCOMP 46 86.8 362 1 1B19_HUMAN HLA CLASS I HISTOCOMP 46 86.8 365 6 MEFX_HUMAN MYOCYTE-SPECIFIC ENHA 46 86.8 368 4 HAIW_MOUSE H-2 CLASS I HISTOCOMP 46 86.8 411 6 INOX_MOUSE PROTEIN-INSINE 6-OXID 46 86.8 411 6 INOX_MAN PROTEIN-INSINE 6-OXID 46 86.8 417 6 INOX_HUMAN PROTEIN-INSINE 6-OXID

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KUDO A., MELCHERS F.;

EMBO J. 6:2267-2272(1987).

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COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX PRESUMABLY REGULARES OF PRE-B-CELLS.

COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY STEPS OF B-CELL DIFFERENTIATION.

C-1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.

C-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

EMBL; X05556; G55410; ...

REMBL; X05557; G55414; ...

REMBL; X05577; G55416; ...

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EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
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01-AN-1990 (REL. 13, LAST SEOUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IMMUNOGLOBULIN IOTA CHAIN PRECURSOR (V(PREB)1 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
45C58A1B CRC32;
                                                                                                                                                                                                                                                                                 15948 MW; ElDA1049 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 3
                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) B-CELL; 5
19
142
41
56
70
70
11
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
               EMBL; M34927; G340305; -.
PIR; S00258; S00258.
HSSP: P01703; LBJL.
MIM; 146770; -.
IMMUNGLOBULIN FOLD; B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.7%;
llarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16125
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                               139 AA;
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 AA;
                                                                                                                                                                                                                                                                                                                                                                                          66 rfllry 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 rfllry 71
                                                                                                                                                                                                                                                                                                                                                                                                                   1 RILLRY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||||
RILLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                             SIGNAL
                                                                                                                                                    DOMAIN
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88196069.

BAUER S. R., VUDO A., MELCHERS F.;

EMBO J. 7:111-116(1988).

-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
STEPS OF B-CELL DIFFERENTIATION.
-!- SIMILARITY: TO MOUSE V(PREB)1 AND V(PREB)2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IMMUNOGLOBULIN IOTA CHAIN PRECURSOR (V(PREB) PROTEIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA: META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                              01-MAY-1992 (REL. 22, CREATED)
1-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANDYATION UPDATE)
PUTATIVE 95.7 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PAU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRESENCE OF A 2N(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER MEDLINE; 92350247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 48; DB 11; Length 832;
llarity 83.3%; Pred. No. 5.28e+00;
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                (1) SEQUENCE OF 1-517 FROM N.A. SEQUENCE OF 1-517 FROM N.A. VAN DER LINDEN C.G., MAURER C.T.C., PLANTA R.J., VAN VLIET-REEDIJK J.C.; SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                           GRENSON M., JAUNIAUX J.-C., URRESTARAZU L.A.;
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 AA.
                                                                                                             832 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 130-832 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDILINE; 88196069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 rillrf 634
628 rillrf 633
                   |||||:
1 RILLRY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 3
VPRE_HUMAN
                                                                                            LT 2
YCZ6_YEAST
P25611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P12018;
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STAN WHY PRINCE OF SERVICE OF SER

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Gaps

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Length 142;

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 2
496 AA;
          90
122
150
225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXIDOREDUCTASE; NAD
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    PSEUDOMONADACEAE.
                                                                                                   202 rvlmry 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rvmlry 72
                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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1 RILLRY
                                                                                                               |:|:||
1 RILLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 8
HAIQ_MOUSE
          TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIT_MET
ACT_SITE
SEQUENCE
                                                                               Matches
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SEQUENCE FROM N.A.

STRAIN-LT2;

MEDLINE; 33.73696.

ROTH J.R., LAWRENCE J.G., RUBENFIELD M., KIEFFER-HIGGINS S., CHURCH G.M.;

J. BACTERROL. 175:33.03-3316(1993).

L. J. BACTERROL. 175:33.03-3316(1993).

L. J. BACTERROL. MAY BE INVOLVED WITH COBALT TRANSPORT IN ASSOCIATION WITH COBALAMIN BIOSYNTHESIS.

LICOBALAMIN BIOSYNTHESIS.

-!- PATHWAY: COBALAMIN BIOSYNTHESIS.

-!- PATHWAY: COBALAMIN BIOSYNTHESIS.

RMBL; L12006; G1544444.

STYCENE; SG10049; CBIO.

RMBL; L12006; G1544444.

RRANSPARMIN BIOSYNTHESIS.

TRANSPEMIN BIOSYNTHESIS; TRANSPORT; TRANSMEMBRANE.

TRANSMEM 65 85 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                             COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY STEPS OF B-CELL DIFFERENTIATION.
-!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
BIRSP, PO1607: 1FGV.
IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                     POTENTIAL.
V(PRED) 2 PROTEIN.
ERAMENORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                           Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING
                                    01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IMMUNGLOBULIN OMEGA CHAIN PRECURSOR (V(PREB)2 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 10; Pred. No. 8.61e+00; 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
6AE40A3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
                    142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 AA
                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK 3
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (REL. 29, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (REL. 31, LAST ANN COBALT TRANSPORT PROTEIN CBIO.
                                                                                                                                                                                                                                                                                                                                                                       16052 MW;
                                                                                                                              SEQUENCE FROM N.A.
STRAIN-DBA/2J X C57BL/6;
MEDLINE; 88029315.
KUDO A., MELCHERS F.;
EMBO J. 6:2267-2272(1987).
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SALMONELLA TYPHIMURIUM.
                                                                                                                                                                                                                                                                                                                                                                       142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                 66 rfllry 71
                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||||
| RILLRY 6
5
VPR2_MOUSE
P13373;
01-,7*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBIQ_SALTY
Q05598;
                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                        MASA_PSEAE STANDARD; PRT; 496 AA.
P28810;
01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P14428;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-Q ALPHA CHAIN (FRAGMENT).
H2-K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEELE M.I., LORENZ D., HATTER K., PARK A., SOKATCH J.R.;
J. BIOL. CHEM. 267:13585-13592(1992).
-!- CATALYTIC ACTIVITY: 2-METHYL-3-OXOPROPANOATE + COA + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                PSEUDOMONAS AERUGINOSA.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA,
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                        Score 47; DB 2; Length 225;
Pred. No. 8.61e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 6; Length 496;
Pred. No. 8.61e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 85206119.
MORITA T., DELARBRE C., KRESS M., KOURILSKY P., GACHELIN
IMMUNOCENETICS 21:367-383(1985).
                     POTENTIAL.
POTENTIAL.
E926FA4B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
4D33C45B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 1-29.
STRAIN=PAO / ATCC 15692;
MEDLINE; 92317087.
   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
110 PC
142 PC
170 PC
25983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 E
53532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                        88.7%;
Similarity 66.7%;
4; Conservative
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RILLRY

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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

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TRYPANOSOMA BRUCEI BRUCEI.
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1986 (REL. 02, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
11-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLIGARE FAMILLE.
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON AND MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
GENERAL ACID (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILAR.
-!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE, 90384806.

BUFRS, R., CORNELISSEN A.W.C.A.;

NUCLEIC ACIDS RES. 18:5089-5095(1990).

-!- CATALYTIC ACTILY: A PHOSPHOPROTEIN + H(2)0 - A PROTEIN +

ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).

-!- TRYPANOSOMA BRUCEI CONTAINS TWO PPI GENES WHICH ARE HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-295.
MEDLINE; 85226361.
EZQUERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
BLOCHEMISTRY 24:1733-1741(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                 01-NOV-1991 (REL. 20, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
SERINE/THREONINE PROTEIN PHOSPHATASE PP1(5.9) (EC 3.1.3.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
IMMUNOBIOLOGY 170:367-380(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 7; Length 346; Pred. No. 1.39e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;
PROC. NATL. ACAD. SCI. U.S.A. 83:1428-1432(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
EMBL, X52746; G10509; -.
PROSITE: PSO0125; SER_THR_PHOSPHATASE.
HYDROLASE: IRON; MANGANESE; MOLTIGENE FAMILY.
                                                                                              346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AA
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25-361 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 86138405.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 90384806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 86149317
                                                                                                                                                                                                                                                                                                                                       TRYPANOSOMATIDAE
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                                                           RESULT 10
PP12_TRYBB
AC
DT 01-NOV-1991
DT 01-FBB-1996
DE SERINE/THREC
DS TRYPANOSOMA
OC TRYPANOSOMA
OC TRYPANOSOMA
OC TRYPANOSOMA
OC TRYPANOSOMA
OC TRYPANOSOMA
RN (1)
RN (1)
RR EVERS R. CC
RL MEDLINE; 903
RA EVERS R. CC
RL ORTHOPHO
CC OTTALYTH
CC -!- TRYPANOS
CC SIMILARI
CC -!- TRYPANOS
CC SIMILARI
CC -!- TRYPANOS
CC -!- TRYPANOS
CC SIMILARI
CC -!- TRYPANOS
CC -!- TRYPANOS
CC SIMILARI
CC -!- TRYPANOS
CC -!- TRY
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1B14_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P03989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-i- SUBDNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2- MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNORATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN (B27-HS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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0
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 1; Length 338;
Pred. No. 1.39e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 4; Length 328; Pred. No. 1.39e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
1; 3845B867 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 AA
                               MICROGLOBULIN).
EMBL, MI4827; G387471; -.
HSSP; P01901; 1VAA.
HSSP; P01901; 1VAA.
"TOTTE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 91268545.
CHOO Y.S., FAN L.A., HANSEN J.A.,
J. INMUNOL. 147:174-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
ilarity 83.3%;
Conservative
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larity 83.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
274
2284
338
338
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259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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1B20_HUMAN
P30467;
                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
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SEQUENCE
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TRANSMEM
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1B18_HUMAN
P10318;
01-MAR-1989 (
01-MAR-1989 (
01-FEB-1995 (
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| RILLRY (
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HA13_MOUSE
P14426;
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1 RILLRY
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DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
DISULFID
CARBOHYD
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SEQUENCE
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                               X-RAY CRYSTALLOGRAPHY.

MEDLINE; 92018187.

MADDEN D.R., GORGA.C., STROMINGER J.L., WILEY D.C.;

MADDEN D.R., GORGA.C.

THE IMMUNE SYSTEM.

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO C. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

-!- DISCASSI THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF ANXLOSING SPONDYLITS.

REMEL; X03945; G32177; ALT_TERM.

R PIR; S07441; S07441.

R PDB; 1HSA: 15-OCT-92.

R PROSITE; PS00290; IG_MHC.

MHC I: TRANSMEMBRANE; GLXCOPROTEIN; SIGNAL; 3D-STRUCTURE.
                                                                                               5
F
       MEDLINE; 92405152.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
CELL 70:1035-1048(1992).
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC TAIL.
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Q -> E (IN REF.
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D-K ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
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                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. IMMUNOL. 119:3878-3885 (1987).

-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-: SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL, M18524; G387453; -.

PROSITE; P01901; 1VAA.

PROSITE; PS00290; IG_MHC.

SIGNAL.

SIGNAL.

J. 24
                                                                                                                                                                                                                                                                                    01-07N-1990 (REL. 13, CREATED)
01-07N-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-K ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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0
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WADLINE; 88060499.
WATTS S. VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
GOODENOW R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 4; Length 362;
Pred. No. 1.39e+01;
0; Mismatches 1; Indels
                                                                                                    Score 46; DB 1; Length 361;
Pred. No. 1.39e+01;
                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
734877E CRC32;
                                                                          40464 MW; 802130D5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                          362 AA.
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                                                                                                      86.8%;
similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                          STANDARD;
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2298
3306
3306
1188
2200
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2200
2200
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275
278
281
288
294
361 AA;
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280
362 AA;
                                                                                                      Query Match
Best Local Similarity
Matches 5; Conser
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(REL.
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9

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P SEQUENCE FROM N.A.

X MEDLINE; 88152906.

A ZEMMOUN J., FENIS P.D., PARHAM P., DUPONT B.;

LIMMUNOGENETICS 27:281-287(1988).

- 1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

- 1- SUBGNIT: DIMEN OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

R MICROGLOBULIN).

R HSSP, F03999; 1HSA.

R MIM: 142890; -.

R PROSITE; PS00290; IG_MHC.

MICROGLOBULIN; SIGNAL.
                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBLLITY ANTIGEN, ALPHA CHAIN BW 47 B4701.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-27 B*2703
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88227491.
CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;
HUM. IMMUNOL. 21:209-219(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-RED-1995 (REL. 31, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBLITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
PRECURSOR (B-27D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1; Length 362;
Pred. No. 1.39e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4, 67734C1E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                          40571 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.8%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICROGLOBULIN).
EMBL; M54883; G187664; -.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                               110
188
283
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115
207
209
310
334
110
125
362 AA;
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| RILLRY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 15
1B16_HUMAN
P19373;
                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
SEQUENCE
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TRANSMEM
DOMAIN
CARBOHYD
DISULFID
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-27 B*2705.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                       3D-STRUCTURE MODELLING OF 115-206.

SOGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;
SUBMITTED (JUL-1994) TO THE PDB DATA BANK.

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1B45_HUMAN STANDARD; PRT; 362 AA.
010.48F-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-47 B*4701 ALPHA CHAIN
PRECURSOR.
   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN PRECURSOR (B-27W) (B27.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                            -i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; X03665; G871297; JOINED.

EMBL; M12967; G187660; ...

EMBL; M12967; HJUBW.

PDB; 1ROG; 30-SEP-94.

PDB; 1ROH; 30-SEP-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 1; Length 362;
Pred. No. 1.39e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN; SIGNAL; 3D-SIRUCTURE.
                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 86138405.
WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER
IMMUNOBIOLOGY 170:367-380(1985).
                                                                                                      SEGUENCE FROM N.A.
MEDILINE; 86220133.
SEEMANN G.H.A. REIN R.S., BROWN C.S., PLOEGH H.L.;
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

7324356 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40428 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                J. S.EP-94.

LUR PDB; 1ROJ; 30-SEP-94.

DR PDB; 1ROX; 30-SEP-94.

DR PDB; 1ROX; 30-SEP-94.

DR PDB; 1ROX; 30-SEP-94.

DR MIM; 142830;

NR PROSITE; PS00230; IG_MHC.

W MHC I; TRANSMEMBRANE; GT.T.

SIGNAL

CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
125
227
362 AA;
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TRANSMEM
DOMAIN
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DOMAIN

Best Loca Matches

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Gaps

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FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40402 MW; 7261C3AB CRC32;
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ö 0; Gaps Query Match 86.8%; Score 46; DB 1; Length 362; Best Local Similarity 83.3%; Pred. No. 1.39e+01; Matches 5; Conservative 0; Mismatches 1; Indels

Db 103 rtllry 108 | 111| Qy 1 RILLRY 6

Search completed: Thu May 22 08:28:09 1997 Job time: 11 secs.

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host

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Example 15; Page 36; 80pp; English.

83016-1883065, R83096 and R82207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIAA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 2.15e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                        Score 42; DB 16; Length 20;
Pred. No. 2.15e+02;
0; Mismatches 1; Indels
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R92911 standard; peptide; 20 AA.
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                        Query Match 79.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                            of the patient.
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Search completed: Thu May 22 08:45:21 1997 Job time: 10 secs. ||| || | YRLLIR 6 ö

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human-leucocyte-associated antigens. This sequence represents the HLA-B2702 84-751/75-84T palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell sufface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by
                                                                              12-NOV-1996 (first entry)
HIA-B2702 84-757/75-84T palindrome.
HIA-B2702 84-757/75-84T palindrome.
HIA-P2702 84-757/75-84T palindrome.
HIA-P2702 84-757/75-84T palindrome.
HIA-P2702 84-757/75-84T palindromen-protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; Syptolysis; antigen presenting cell.
WQ9513288-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                       Compsns. comprising lymphoid surface membrane proteins - which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example; Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                         inhibit cytolytic activity and differentiation of CTLs. Example: Page 12; 29pp; English.
R95413, and R95415-R95431 represent palindromes and fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 18; Pred. No. 2.15e+02;
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .T. 6
R95430 standard; peptide; 20 AA.
R95430;
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imilarity 83.3%;
5; Conservative
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WPI; 95-194027/25.
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of a coeptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                          HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytockoit Tlymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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Cytockoic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                  Gaps
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mix the extracellular portion of p74, in an amount compete with p74 for the binding of the p74 ligand. AA;
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05-APR-1994; US-222851.
05-APR-1994; US-222851.
Clayberger C. Krensky AM, Parham P;
WPI; 95-358882/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 2.15e+02;
0; Mismatches 1; Indels
                                                                                                   Length 20;
                                                                                                                                                Indels
                                                                            Score 42; DB 18; Len
Pred. No. 2.15e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parham P;
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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larity 83.3%;
Conservative
                                                                                                79.2%;
83.3%;
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                                                                                                                                                Conservative
                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
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WPI; 95-358582/46.
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  25 the
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WO9526979-A1.
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adding to th
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                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                           R92907;
                                                                                                                                             Matches
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12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
HIA-12702 84-79-84 palindrome.
HIA-1274: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
Synthesic:
W09513288-A1.
                                                                                                                                                                                                                                                                                       18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(S-ND ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                    standard; peptide; 12 AA.
                3 ynllir
                                                                                                                  R95429 s
R95429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                셤
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                                                à
                                                         Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities sample 2, Page 67-68; 146pp; English.

RR742-R87144 represent partial fragments of the drosophila protocadherin sequence. The cDNAs encoding these sequences were isolated after sequence. The cDNAs encoding these sequences were isolated after consequences of the third and fourth extracellular domains of the amino acid sequences of the third and fourth extracellular domains of the canno acid sequences of the third and fourth extracellular domains of the interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain of cadherins adhesive function. The cadherins and ont possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cell-cell adhesion. These sequences may have regulatory functions in the cell. These protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.

Example 5: Page 109: 138pp; English.

Example 5: Page 109: 138pp; English.

R59496-R61666 are immunogenic 10mer peptides that contain a HIA-A2.1 binding motif. These peptides bind HIA-A2.1 and have a binding affairty of at least 1% as compared to a reference peptide (R71293). R61548 has an 1050 of 0.0036 and the sequence occurs at position 24 in the HPV E6 protein. The peptides of the invention can induce cytocoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydr-1995 (first entry)
Peptide fragment (1.0914) of HPV binds HLA-A2.1.
Peptide fragment (1.0914) of HPV binds HLA-A2.1.
Autigen; eptitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HWU; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen-1; core antigen; surface antigen; core antigen; surface antigen; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; Smer; lomer; anchor; human leukocyte antigen.
W09420127-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 17; Length 43;
Pred. No. 7.66e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 11; Length 10;
Pred. No. 1.66e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grey HM, Kast WM, Sette A, Sidney J;
WPI; 94-302678/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .r 3
R61548 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.18;
Similarity 83.38;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1994; U02353.
05-MAR-1993; US-027146.
04-UUN-1993; US-073205.
29-NOV-1993; US-159184.
(CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer or lymphoma, etc.
(DOHE-) DOHENY EYE INST
                              96-068873/07.
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                                              N-PSDB; T03617
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                 Suzuki
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Wri; yo-19402//20.

PT Composits of Imphoid surface membrane proteins - which may composits comprising lyaphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HA-B2702 84-79-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane communion associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein R970.

CC protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein R970.

CC protein associated mumber of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity expressed on B and T cells. p74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity coll with a suit of the sextracellular fragment of p74 combined with the extracellular portion of cri activity can be inhibited in a cellular composition of containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R95428;
12-NOV-1996 (first entry)
HIA-B3702 84-75-84 palindrome.
B cell; calculum influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 18; Length 12;
Pred. No. 2.15e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1995.
10-NOY-1994; U12985.
10-NOY-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R95428 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.2%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WO9513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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Gaps

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Best Local Similarity

Matches

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using Smith-Waterman algorithm protein - protein database search, MPsrch\_pp

Thu May 22 08:45:11 1997; MasPar time 1.73 Seconds 37.783 Million cell updates/sec Run on:

not generated Tabular output >US-08-653-294-6 (1-6) from US08653294.pep 53

Description: Perfect Score: Sequence:

1 YRLLIR 6 PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

a-geneseq26 Database:

i.parti 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7 8.part8 9.part9 10.part10 11.part11 12.part12 13.part13 14.part14 15.part15 16.part16 17.part17 18.part18 19.part19

Mean 16.490; Variance 45.535; scale 0.362 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	7.66e+01	7.66e+01	٠.	2.15e+02		2.15e+02			2.15e+02
Description	Drosophila-12 cadher		Peptide fragment (1.0	HLA-B2702 84-79-84 pa	HLA-B2702 84-75-84 pa	HLA-B2702 84-75T/75-8	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat
a	R58902	R87142	R61548	R95429	R95428	R95430	R92907	R92909	R92911
DB	11	17	11	18	18	18	16	16	16
* Query Match Length DB	43	43	10	12	70	20	20	20	20
* Query Match	86.8	86.8	81.1	79.2	79.2	79.2	79.2	79.2	79.2
ult No. Score	46	46	43	42	42	42	42	42	42
Result No.	1	7	m	4	'n	Q	7	ω	σ

Note: Post-processor removed 36 summaries from list due to search parameters chosen.

# ALIGNMENTS

R58902 standard; Protein; 43 AA. R58902; 17-APR-1995 (first entry RESULT SAF

Natural S;

Natural S;

Natural S;

Natural S;

Natural S;

Natural S;

Naturation actual binding and regulating activities.

Polynucleotide sequences encoding new proto:cadherins - useful
For modulating natural binding and regulating activities.

Example; Page 63; 114pp; English.

Two regions of conserved AA sequence, one from the middle of the curth extracellular subdomain (EC-3) and the other from the chiral cadherin extracellular subdomain (EC-4) were designed for use as PCR primers. PCR was carried out on a rat brain conversion of the fourth extracellular subdomain (EC-4) were designed for use as PCR primers. PCR was carried out on a rat brain conversion of the previously identified about 450 bps and 130 bps were found.

The 450 bp band corresponded to the expected length between the two primer sites, but the 130 bp band could not be predicted from any coff the previously identified cadherin sequences. The 450 bp and 130 bp band could not be predicted from any coff the previously identified cadherin sequences. The 450 bp and 130 bp band sequences. Or the PCR primers of the Clones were isolated. The DNA and deduced AA sequences of the resulting PCR fragments structurally similar to the rat cDNAs were isolated from human, mouse and Xenopus brain cDNA prepns. By PCR using the above primers.

Cholouds whole body cDNA prepns. by PCR using the above primers.

Che bnA and deduced AA sequences of the resulting PCR fragments (including sequences corresp. to the PCR primers) are given in preparation of the deduced AA sequences indicates a similarity, in particular, there are three sets of clones that appear to be cross-species homologues: RAT-218, MOUSE-325 and HUMAN-43; RAT-314, MOUSE-321 and HUMAN-11; and MOUSE-326 and HUMAN-42. ö Length 43; 0; Indels Score 46; DB 11; I Pred. No. 7.66e+01; 1; Mismatches 0; Cadherin, sell adhesion molecule, Drosophila, WQ9414960-A, Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative 07-JUL-1994. 23-DEC-1993; U12588. 29-DEC-1992; US-998003. (DOHE) DOHENY EYE INST. Suzuki S; yrlvir 16 9 |||:|| | YRLLIR 11 셤 ò

Gaps

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29-AUG-1996 (first entry)

Protocadherin clone DROSOPHIIA-12.

Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly. T R87142 standard; Peptide; 43 AA.

RESULT

Location/Qualifiers Misc\_difference 39
/note= "encoded by Arg"
Misc\_difference 40
/note= "encoded by AcA"
/note= "encoded by AcA" Drosophila melanogaster Misc\_difference Key 

ဦပ္ပင္ပ W09600289-A1. 04-JAN-1996. 26-JUN-1995; U08071. 27-JUN-1994; US-268161. /note= "encoded by A7 Misc\_difference 42 /note= "encoded by C4 Misc\_difference 42 /note= "encoded by C6 Misc\_difference 43 /note= "encoded by C6

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:26:43 1997; MasPar time 2.78 Seconds 61.517 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-4 (1-6) from USO8653294.pep 49 Title: Description: Perfect Score:

1 RIALRY 6 Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 21.604; Variance 27.804; scale 0.777 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00	3.39e+00
Description	MHC class I bistocom	MHC class I histocom	HLA-B38	class I histocompati	MHC class I histocom	gene HLA B-1517 prot	MHC HLA-B transmembr	HLA-Bw57.2 antigen -	transmembrane glycop	lymphocyte antigen	MHC class I histocom	MHC class I histocom	MHC class I histocom	class I histocompati	class I histocompati	MHC class I histocom	class I histocompati				
А	I38509	HLHU32	I54463	I59308	180168	180167	180171	180169	HLHU12	I62045	I59633	137521	I84486	I84490	A45834	HLHUB8	B30345	JH0541	JH0540	A30345	524434
DB	13	~	13	13	13	13	13	13	~	13	13	13	13	13	ø	~	9	9	9	ø	9
% Query Match Length	273	274	274	354	354	354	355	355	359	362	362	362	362	362	362	362	362	362	362	362	362
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	49	49	49	49	49	49	4	49	49	49	49	49	49	49	49	49	40	49	49	49	49
Result No.	П	7	e	4	ស	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21

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### ALIGNMENTS

RESULT 1 ENTRY	138509 *type fragment
TITLE ORGANISM DATE	MHC class I histocompatibility antigen - human (fragment) #formal_name Homo sapiens #common_name man 06-Sep-1996 #sequence revision 06-Sep-1996 #text change
ACCESSIONS	91
REFERENCE #authors	I38509 Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal	lens (1994) 44:271-273
#title #cross-refer	#title HLA-B*5105, a newly identified B51 IEF variant.
#accession	138509
##status ##molecul	##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA
##residues ##cross-re	##residues 1-273 ##label RES ##cross-references EMBL:U06697; NID:q469544; CDS_PID:q469545
GENETICS	
#note SUMMARY	gene name HLA-B #length 273 #checksum 6533
Query Match Best Local Si	similarity 100.0%; Score 49; DB 13; Length 273; Similarity 100.0%; Pred. No. 3.39e+00;
səı	0; Misma
Db 78 rialry	y 83
Qy 1 RIALRY	9 - 14
RESULT 2	
ENTRY TITLE	HLHU32 #type fragment MHC class I histocompatibility antigen HLA-A32 alpha chain -
· MOINTOGO	
DATE	#101md1_name nome sapiens #common_name man 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 06.com.1006
ACCESSIONS REFERENCE	A26088 A26088 A26088
#authors	Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
#Journal #title	J. Immunol. (1986) 13/35/1-35/4 The primary structure of HLA-A32 suggests a region involved
#cross-refer	in formation of the Bw4/Bw6 epitopes. #cross-references MUID:87058961
#accession	A26088

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#length 354 #checksum 3211
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Welss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title Genetic and serological heterogeneity of the supertypic HLA-B locus specificities Bw4 and Bw6.
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#journal Proc. Natl. Acad. Scl. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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MHC HLA-B38 chain - human (fragment)
#formal_name Homo sapiens #common_name man
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##molecule_type DNA # #label RES 1-274 ##label RES #stross-references GB.M29864; WID:9187674; CDS_PID:9187675 X #length 274 #checksum 1031
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##molecule_type protein
##residues 1-274 ##label WAN
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A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross.references WUID:94286544
#accession 180167
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Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
Exon/intron organization and complete nucleotide sequence of
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#formal_name Pan troglodytes #common_name chimpanzee (fragment) 24-May-1996 #sequence_revision 24-May-1996 #text_change 180171
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AMNISM #formal_name Pan troglodytes #common_name chimpanzee

24-May-1996 #sequence_revision 24-May-1996 #text_change
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FRENCE McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897

#title A uniquely high level of recombination at the HLA-B locus.
                                                                                                               #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
    A.L.; Bontrop, R.E.; Wakkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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#formal_name Homo sapiens #common_name man
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MHC class I histocompatibility antigen HLA alpha chain
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##residues 1-359 ##label MAL
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#product class I histocompatibility antigen HLA alpha
Chain #status predicted #label MAT/
#domain extracellular #status predicted #label EXT/
#domain alpha-1 #label EXI/
#domain alpha-2 #label EXI/
#domain immunoglobulin homology #label IMM/
#domain intransmembrane #status predicted #label IMM/
#domain intracellular #status predicted #label IMM/
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Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
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22/1; 112/1; 204/1; 296/1; 335/1; 346/1
#superfamily class I histocompatibility antigen;
immunoglobulin homology
duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
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#length 362 #molecular-weight 40417 #checksum 7730
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##molecule_type mRNA
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Pred. No. 3.39e+00;
0; Mismatches 0; Indels
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Pred. No. 3.39e+00;
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Best Local Similarity 100.0%;
Matches 6; Conservative
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#authors Hildebrand, W.H.; Domena, J.D.; Parham, P.
#journal Tissue Antigens (1993) 41:190-195
#title Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and
#cross-references MUID:93369833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title
#cross-references MUID:94367483
#accession 184486
                                                                                                                                                                                                                                                                            Gaps
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transmembrane glycoprotein - human
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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HIA-BW57.2 antigen - human
#formal_name Homo sapiens #common_name man
02.Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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#length 362 #molecular-weight 40584 #checksum 8821
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##residues 1-362 ##label RES
##cross-references EMBL:X61707; NID:932186; CDS_PID:932187
XX #length 362 #molecular-weight 40342 #checksum
                                                                                                                                  ##residues 1-362 ##label RES ##cross-references GB:L07743; NID:g388314; CDS_PID:g388315
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#molecule_type mRND
##residues
##cross-references GB:L15005; NID:9493154; CDS_PID:9493155
                                                                                          ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
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Pred. No. 3.39e+00;
0; Mismatches 0; Indels
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Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.;
Takiguchi, M.
Immunogenetics (1990) 32:195-199
Allospecificities between HIA-Bw53 and HIA-B35 are generated
by substitution of the residues associated with HIA-Bw4/Bw6
public epitopes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.;
Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.;
Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P.
#journal Tissue Antigens (1995) 45:177-187
#title The HAA-A.B.C genotype of the class I negative cell line
Daudi reveals novel HLA-A and -B alleles.
                                                                                                                                          Gaps
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
gene name HLA-B*1513
#length 362 #molecular-weight 40378 #checksum 9463
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#length 362 #molecular-weight 40355 #checksum 8277
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#map_position 6p21.3-6p21.3
CLASSIFTCATION #superfamily class I histocompatibility antigen;
KEYWORDS heterodimer; transmembrane protein
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##molecule_type mRNA
###molecule_type mRNA
                                                                                    Length 362;
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Pred. No. 3.39e+00;
0; Mismatches 0; Indels
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##cross-references GB:M58636; GB:M33574
##note this allele is designated B*5301
                                                                              Score 49; DB 13; I
Pred. No. 3.39e+00;
0; Mismatches 0;
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ymphocyte antigen -
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#domain signal sequence #status predicted #label SIGN
#domain immunoglobulin homology #label IMMN
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 362 #molecular-weight 40495 #checksum 9558
FEATURE
1-24
220-285
110
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SUMMARY

0; Gaps Query Match 100.0%; Score 49; DB 6; Length 362; Best Local Similarity 100.0%; Pred. No. 3.39e+00; Matches 6; Conservative 0; Mismatches 0; Indels

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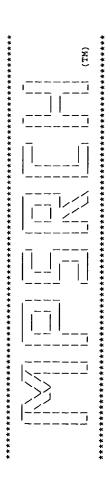
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Search completed: Thu May 22 08:27:07 1997 Job time: 24 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:27:25 1997; MasPar time 1.93 Seconds 33.906 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-4 (1-6) from US08653294.pep 49 Title:

1 RIALRY 6 Description: Perfect Score: Sequence:

92623 seqs, 10896596 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-geneseq26 Database:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19

Mean 15.638; Variance 39.027; scale 0.401 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	8	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01	+01
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	Description	Alphal-helix of HLA-B	HLA-B2702.75-84(D).	Peptide fragment of C	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 84-79-84 pa	HLA-B2702 CTL modulat	HLA-B2702 84-75-84 pa	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702.60-84.	HLAB38.6084.	HLA-B2702 CIL modulat	Peptide fragment of C	HLAB38 CTL modulating	Peptide fragment of H	HLA-Bw53 exon.	Sequence of HLA-Bw52	Sequence of HLA-B51 a	pJH1 gene product - b
	A	R95413	R95425	R41208	R83062	R83094	R95429	R92912	R95428	R92907	R92908	R95416	R95422	R83090	R41205	R83093	R48286	R12463	R03142	R03144	R04104
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3.03e+01		3.03e+01	•	3.03e+01	•	٠	٠	4.07e+01		Ψ.	٠	9.64e+01	9.64e+01	9	φ.	9.64e+01	ď	7	~	~	1.28e+02	1.28e+02	1.28e+02	1.28e+02
G-protein coupled dog		adenosin		Human ventricle A2a a	Human A2a adenosine r		PB145 serpin enzyme c	Yeast MSH1 protein.	Yeast MSH1 protein wi	02.75-84(T).			HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	Cardiac adenylyl cycl	n polype	tei	denosine	Human Al adenosine re	Human Al adenosine re	Al adenosine receptor	Human ventricle Aī ad	ŏ	Hsp70 antigen of Myco
5	m	R47387	-	R93990	~	R87656	N	90	R76070	R95426	R83096	R83095	R92910	R92909	R37309	R44431	W02659	R45744	R41524	R47386	O		38	R05874
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### ALIGNMENTS

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copions compositions competed to the extracellular flux. This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein prof from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell lysate. P74 is a T-cells, and is also immunologically cross reactive with the heat shock protein and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity compositions comprising the extracellular fragment of F74 combined with HzA-B2702.60-84 (see R95416), induces calcum influx, and inhibits compositions comprising the extracellular fragment of F74 combined with HzA-B2702.60-84 (see R95416), induces calcum influx, and inhibits compositions and be screened for their effect on the cytolytic activity of T-cells, by combining the mount of binding between the candidate compound and F74. Modulation of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition with the extracellular portion of F74, in an amount sufficient to compete with F74 for the binding of the F74 ligand.
                                                                12-NOV-1996 (first entry)
Alphal-helix of HIA-B3702.
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Compons. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example; Page 11; 29pp; English.

This sequence represents the alphal-helix of the
                                                                                                                                                                                                                                                                                 18-MAX-1995.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                    cytolysis; antigen presenting cell.
                     R95413 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                              Synthetic.
WO9513288-A1.
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RESULT
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Query Match 100.0%; Score 49; DB 18; Length 10; Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Gaps

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0; Indels

US-08-653-294-4.rag

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16-WAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of The peptides are administered to a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the pifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILs
                                              Mew peptide(s) based on class I HLA antigen domains - used for modulating cytocxic T-lymphocyte activity towards targets claim 11; Page 54; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R83094 standard; peptide; 10 AA.
R83094;
R16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                               Score 49; DB 8; Length 10;
Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0;
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 STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R83062 standard; peptide; 10 AA.
R83062;
                                                                                                                                                                                                                                                                                             / Match
Local Similarity 100.0%;
les 6; Conservative
                     Krensky AM;
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Local Similarity 100.0%;
6; Conservative
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 UNIV LELAND
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WPI; 95-358582/46.
(STRD ) UNIV LELAN
Clayberger CA, Kr
WPI; 93-303134/38.
                                                                                                                                                                                                                                                              10 AA;
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Composins. comprising lymphoid surface membrane proteins - which may finhibit cytolytic activity and differentiation of CTLS.

Frample: Page 11: 29pp: English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the H1A-B2702.75-84(D). These sequences can be used to isolate the protein of sociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on English and teargent, and then passed through an affinity column corrected extracellular fragment of P74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolytic activity of compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate compound and P74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of P74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the seminance of the p74 ligand.
                                                                                                                                                              12-NOV-1996 (first entry)
HLA-B2702.75-84(D).
HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; HSC70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
Cytolysis; antigen presenting cell.
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 Gaps
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Human leukocyte antiqen: HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.

Synthetic.
W09317699-A.
16-SEP-1993.
25-FEB-1993; U01758.
02-MAR-1992; US-844716.
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 Mismatches
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM:
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181208 standard; peptide; 10 AA.
181-WAR-1994 (first entry)
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R95425 standard; peptide; 10
R95425;
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Best Local Similarity 100.0%;
 Conservative
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| RIALRY
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Length 10;

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Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
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Local Similarity 100.0%;
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05-APR-1995; U04349.
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WPI, 95-358582/46.
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WPI; 95-194027/25
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WHI: 95-194007/25.

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                                                                                                                                                                                                                                                         R83061-R83085, R83090-R8309 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the petide for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CILS)
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HIA-B3702 84-79-84 palindrome.
HIA-B3702 84-79-84 palindrome.
HIA-B3702 84-79-84 palindrome.
HIA-PA-B3702 84-79-84 palindrome.
HIA-PA-B3702 84-79-84 palindrome.
HIA-PA-B4-84 alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
Synthetic.
W09513288-A1.
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 graft versus host disorder; transplantation; therapy;
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                                                                                                                                                     Krensky AM, Parham P;
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                             STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                             Example 14; Page 34; 80pp; English
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R95429 standard; peptide; 12 AA.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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immunosuppressant; gra
class I MHC; HLA-B2702
                                                                                                            US-222851
                                                                          05-APR-1995; U04349
05-APR-1994; US-2228
                                                                                                                                                 Clayberger C, Krei
WPI; 95-358582/46.
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||RIALRY 6
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                     class I
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ESULT 8

ID R95428 standard; peptide; 20 AA.

ID R95428 standard; peptide; 20 AA.

XG R95428.

3T 12-NOV-1996 (first entry)

DE HLA-B2702 84-75-84 palindrome.

KW HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lygate; membrane protein; mammal; heat shock protein; Hsc70; APC;

KW Cytolysis; antigen presenting cell. lymphocyte; CTL; differentiation;

KW Cytolysis; antigen presenting cell.

NO9513288-A1.

PD 10-NOV-1995; US-1595.

PF 10-NOV-1995; US-15949.

PR 110-NOV-1995; US-15949.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
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R83061-R83085, R83090, R831096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly
containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.70-84).
CYtotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
imminosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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Pred. No. 1.25e+01;
0; Mismatches 0; Indels
                                                                                                                                                                               Score 49; DB 18; Length 12;
Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92912 standard; peptide; 15 AA.
R92912;
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92807-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a The peptides are administered to a patient. This is administered to
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T Lymphocyte; CTL; major histocompatibility complex; MHC; immuosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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                                                                                                                                                                                                                                                                                                            Score 49; DB 18; Length 20;
Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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12-0C1-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92907 standard; peptide; 20 AA.
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Best Local Similarity 100.0%;
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Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abanch the patient for a limited period of time (comparad to Histerime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CLLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composine. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 9; 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents HLA-B2702.60-84. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1996 (first entry)
HIA-B2702.60-84.
HIA-B2702.60-84.
HIA-D4: plyal-helix; human-leucocyte-associated antigen; inhibitor;
HIA- p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                  16-MAY-1996 (first entry)

HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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    Mismatches

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(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                            05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                      standard; peptide; 20 AA
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10-NOV-1994; U12985.
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WPI; 95-358582/46.
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12-NOV-1996
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Pred. No. 1.25e+01;
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Best Local Similarity 100.0%; Matches 6; Conservative

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R83090 standard; peptide; 25 AA.
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PT Inhibit cytolytic activity and differentiation of Cris.

PS Example's Page 9: 29p; English.

CR 895413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HAB38.6084. These sequences can be used to isolate the protein p74 from a T-cell lyate. P74 is a T-cell surface membrane protein massociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70. P74 is found in a cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

Containing a covalently bound HIA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising them with the extracellular portion of p74 and determining the amount of binding between the candidate composition of CT activity can be inhibited in a celluar composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete companence of the p74 ligand.
amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.
Compositions comprising the extracellular fragment of p74 combined with this sequence, induces calcium influx, and inhibits cytochort T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing r-cells and antignen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane profesh; mamman.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 18; Length 25; Pred. No. 1.25e+01; 0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0;
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10-NOY-1994; U12985.
10-NOY-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B cell; calcium influx; cytotoxic T cytolysis; antigen presenting cell.
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R95422 standard; peptide; 25 AA.
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Matches 6; Conservative
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Matches 6; Conservative
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Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompetibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subcherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
HLA-B2702 CTL modulating peptide (B2702.60-84).
Cytockoic T lymphocyte; CTL; major histocompatibility complex; MHC;
imminosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytocoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and mooplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
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R41205;
R41205;
15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic I lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.25e+01;
0; Mismatches 0;
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Pred. No. 1.25e+01;
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05-APR-1994; UG-222851.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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WPI; 95-358582/46.
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WPI; 93-303134/38
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PR 067-A2995. U04349.

12-0CT-1995.

US-APR-1995; U04349.

PR 05-APR-1995; U04349.

PR 05-APR-1995; U04349.

PR 05-APR-1995; U04349.

PR 05-APR-1995; U04349.

Clayberger C, Krensky AM, Parham P;

DR WP1: 95-358580746.

PT Clayberger C acceptance period of transplants from MHC unmatched of acceptance period of transplants from MHC unmatched of acceptance period of transplants from MHC unmatched of acceptance period of the alpha-1 domain of the recipient processon of acceptance corresponds to residues 60-84 of the alpha-1 domain of the class I MHC class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC class I major histocompatibility complex (MHC) antigens. The peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a current treatments). The peptides particularly modulate (or inhibit) the current treatments). The peptides particularly modulate (or inhibit) the cativity of the cytotoxic T lymphocytes (CTLs) of the patient.
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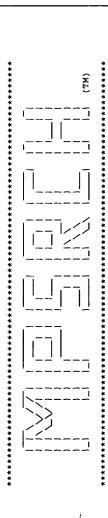
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu May 22 08:28:27 1997; MasPar time 2.70 Seconds 63.421 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-5 (1-6) from US08653294.pep 53 Title: Description: Perfect Score:

1 RILLRY 6 Sequence: PAM 150 Gap 15 Scoring table:

89912 segs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pirso 1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Mean 22.859; Variance 32.635; scale 0.700 Statistics:

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00000000000000000000000000000000000000	11	S25198	vacuolar membrane pr	2.39e+01
		S19418	probable membrane pr	2.39e+01
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	13	S00258	VpreB protein - huma	3.57e+01
88888888888888888888888888888888888888		A28344		3.57e+01
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88888 8999 8988 8988 8988 8988 8988 89	3 14	I54414	MHC H-2K transplanta	5.29e+01
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riosus	3.4) - Pyrococcus furiosus	#type complete endopeptidase (EC 3.4 rotein	#ty pep		JC4084 prolyl mlr-2 p		1 S_NAMES	RESULT 1 ENTRY TITLE ALTERNATE_NAMES	
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1.14e+02	S6 protein kinase -	A53300	14	735		83	44		
Ť	growth factor-stimul		13	733	0	83	44	44	
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7.		A33165	175	1203		8	45	41	
.79	ribosomal protein S3	S53849	12	298		84	45	40	
۲.	protein	807359	ω	218		84	45	39	
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5.29e+01	DNA topoisomerase (A	A39242	o y	1626		80	40	900	
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	DNA topoisomerase (A	S59969	16	1612		86	46	34	
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~	ein-lysine	OXRIL	7	411		86	46	29	
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5.29e+01	serum response facto	A39481	13	365		8 6	9 4	9 6	
	human lymphocyte ant	137485	13	362		86	46	25	
	MHC HLA-B27d - human	I54289	13	362		86	46	24	
•	MHC class I histocom	HLHUB2	7	362		86	46	23	
5 29e+01					٠	3	0	77	

JC4084 #type complete prolyl endopeptidase (EC 3.4) - Pyrococcus furiosus mlr-2 protein 12-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Mar-1996	Mobinson, K.A.; Bartley, D.A.; Robb, F.T.; Schreier, H.J. Gene (1995) 152:103-106 A gene (1995) 152:103-106 A gene from the hyperthermophile Pyrococcus furiosus whose deduced product is homologous to members of the prolyl oligopeptidase family of proteases.  JC4084 Lype DM 1-616 ##label ROB erences GB:U08343 hydrolase; oligopeptidase	Site Ser, Asp, His #status predicted #molecular-weight 70867 #checksum 9939 #molecular-weight 70867 #checksum 9939 s; Score 51; DB 10; Length 616; s; Pred. No. 6.99e+00; s 1; Mismatches 0; Indels 0; Gaps 0;	vacuolar membrane protein HMT1 - fission yeast vacuolar membrane protein HMT1 - fission yeast (Schizosaccharomyces pombe) 4.6chizosaccharomyces pombe 28-May-1993 #sequence_revision 28-May-1993 #text_change 20-Jan-1995 25198 25198 25198 Cortiz, D.F.; Kreppel, L.; Speiser, D.M.; Scheel, G.; McDonald, G.; Ow, D.W. EMBO J. (1992) 11:3491-3499 Haavy metal tolerance in the fission yeast requires an
JC4084 #type complete prolyl endopeptidase (EC 3.4 mlr-2 protein #formal_name Pyrococcus furiosus 12-Jul-1995 #sequence_revision 0 21-Mar-1996	Mobinson, K.A.; Bartley, D.A.; Robb, Gene (1995) 152:103-106 A gene from the hyperthermophile Pyrodect of product is homologous to milligopeptidase family of proteases JC4084 Lype DMA	#active_site Ser, Asp, His th 616 #molecular_weight 7 96.2%; Score 51; DB 10 y 83.3%; Pred. No. 6.99e+ ervative 1; Mismatches	s25198 *type complete vacuolar membrane protein HMT1 - fissi, '(Schizosaccharomyces pombe; 28-May-1993 *sequence_revision 28-May- 20-Jan-1995 \$25198 \$25198 \$25198 \$25198 \$25198 \$25198 \$25198 \$25199 In 1992
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RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE	KEFERENCE #Journal #Journal #title #accession ##molecule ##residues ##residues ##residues FEATWORDS	477,561,592 #lengt.  Query Match Best Local Similarity Matches 5; Conse Db 334 rvllry 339  :     Qy   RILLRY 6	RESULT 2 ENTRY TILE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title

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ATP-binding cassette-type vacuolar membrane transporter. 525198
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#length 830 #molecular-weight 94007 #checksum 7697
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probable membrane protein YCR106w - yeast (Saccharomyces
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31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
12-May-1995
519418: S19747
519415
van der Linden, C.G.; Maurer, C.T.C.; Planta, R.J.; van
Vliet-Reedijk, J.C.; Vreken, P.
submitted to the Protein Sequence Database, March 1992
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Pred. No. 2.39e+01;
1; Mismatches 0; Indels
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##cross-references EMBL:X59720
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##cross-references EMBL: 214055
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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ATP binding;
                                   ##molecule_type mRNA
##residues 1-83(
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#length 142 #molecular-weight 16125 #checksum 8179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Mus musculus #common_name house mouse 19-May-1989 #sequence_revision 19-May-1989 #text_change 23-Mar-1993 #84844 A91077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kudo, A.; Melchers, F. EmBO J. (1987) 6:2267-2272 A second gene, Vprea in the lambda-5 locus of the mouse, which appears to be selectively expressed in pre-B
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Pred. No. 3.57e+01;
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VpreB protein precursor - mouse
#type complete
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##residues 1-139 ##label BAU
##cross-references EMBL:M34927
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#map_position 22q11.2-22q11.2
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##molecule_type DNA
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                                                                                                                                                                                                                  1-142 ##label KUD the authors translated the codon GAG for residue 110 as _{\rm Gln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
J. Biol. Chem. (1992) 267:13585-13592
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                                                                                #authors Kudo, A.; Melchers, F.
#journal EMBO J. (1987) 6:2267-2272
#title A second gene, VpreB in the lambda-5 locus of the mouse,
which appears to be selectively expressed in pre-B
| Jymphocytes |
#cross-references MUID:88029315
                                                                                                                                                                                                                                                                                        MAT
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#formal_name Mus musculus #common_name house mouse
19-May-1989 #sequence_revision 19-May-1989 #text_change
23-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
157832
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Fougereau, M.; Schiff, C.
Mol. Immunol. (1994) 31:1099-1108
#title The human pre-B cell receptor: structural constraints tentative model of the pseudo-light (psi L) chain.
#cross-references MUD:95021318
#accession 157832
                                                                                                                                                                                                                                                                                    #product VpreB protein #status predicted #label
#length 142 #molecular-weight 16052 #checksum 7379
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##cross-references GB:S74019; NID:9693810; CDS_PID:9693811
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Pred. No. 3.57e+01;
1; Mismatches 0; Indels
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#length 145 #molecular-weight 16605
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/Pre-B protein - human
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ilarity 83.3%;
Conservative
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Similarity 83.3%;
5; Conservative
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##molecule_type DNA
##residues 1-14
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Matches 5; Conser
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| RILLRY 6
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1-168 ##label CRO
the mature protein was determined after unblocking; the nature of the blocking group was not determined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
# title A uniquely high level of recombination at the HLA-B locus. #accession 180174
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protein-lysine 6-oxidase (EC 1.4.3.13) - pig (fragments)
lysvl oxidase
#formal_name Sus scrofa domestica #common_name domestic p
27-oct-1995 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
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Biochem. J. (1995) 306:279-284
The proteolytic processing site of the precursor of lysyl
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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#title Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-hydroxyisobutyrate dehydrogenase.#cross-references WID:92317087
                                                                                                                                                                                                                                                     #Superfamily aldehyde dehydrogenase (NAD+)
oxidoreductase
#length 497 #molecular-weight 53663 #checksum 4590
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.X #length 137 #checksum 5064
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Pred. No. 5.29e+01;
0; Mismatches 1;
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Pred. No. 3.57e+01;
2; Mismatches 0;
                                                                                                                                                             ##residues 1-497 ##label STE #cross-references EMBL:M84911; NCBIP:107707
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##residues the protein
1-168 ##label
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##residues
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larity 83.3%;
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66.7%;
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#journal J. Immunol. (1992) 148:4043-4053
#title HLA-J, a second inactivated class I HLA gene related to HLA-G
and HLA-A. Implications for the evolution of the
HLA-A-related genes.
#cross-references WID:92291530
#accession I72808
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MHC class I histocompatibility antigen RT-BM1 alpha chain
rat (fragment)
#formal_mene Rattus norvegicus #common_name Norway rat
03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
A45840
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HIA-B37 M2+ - human (fragment)
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Uul-1996
155965
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#journal J. Immunol. (1986) 137:2168-2172
#title Absence of polymorphism between HLA-B27 genomic exon
sequences isolated from normal donors and ankylosing
#cross-references MUID:87009855
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##molecule_type DNA
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Immunogenetics (1990) 31:211-214
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Pred. No. 5.29e+01;
0; Mismatches 1;
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Pred. No. 5.29e+01;
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Similarity 83.3%;
5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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##residues 1-2
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Best Local Similarity
Matches 5; Conserv
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       using molecular oxygen catalyzes the oxidative deamination of peptidyl-lysine to peptidyl-allysine, ammonium and hydrogen
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##experimental_source K1, strain EV1
##note sequence inconsistent with the nucleotide translation
##note sequence extracted from NCBI backbone
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MHC class I HLA-J antigen - human
#formal_name Homo sapiens #common_name man
02.Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02.Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                      neuE protein - Escherichia coli (fragment)
#formal_name Escherichia coli
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.
#journal J. Bacteriol. (1992) 174:1099-1108
#title Functional analysis of the sialyltransferase complexes.
Escherichia coli Kl and K92.
#cross-references MUID:92138601
                                                                                                                                          #modified_site blocked amino end (Asp) #status
                                                    collagen biosynthesis; elastin biosynthesis #superfamily protein-lysine 6-oxidase blocked amino end; copper; extracellular protein; glycoprotein; oxidoreductase; quinoprotein
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S21890
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Pred. No. 5.29e+01;
2; Mismatches 0; Indels
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Pred. No. 5.29e+01;
2; Mismatches 0;
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#length 168 #checksum 7344
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##molecule_type DNA
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A42644; S21890
A42644
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity 66.7%;
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154414 #type fragment
MMC H-2K transplantation antigen - mouse (fragment)
MMC Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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Morita, T.; Delarbre, C.; Kress, M.; Kourilsky, P.; Gachelin,
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#title An H-2K gene of the t-w32 mutant at the T/t complex is
close parent of an H-2K-q gene.
#cross-references wIUD:85206119
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##molecule_type mRNA
##residues 1-328 ##label RES
##cross-references GB.M14827; NID:9199550; CDS_PID:9387471
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                                     Score 46; DB 6; Length 284;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 1.90 Seconds 34.326 Million cell updates/sec Thu May 22 08:29:04 1997; Run on:

Tabular output not generated.

>US-08-653-294-5 (1-6) from US08653294.pep 53 Description: Perfect Score:

1 RILLRY 6 Sequence:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq26 Database:

|:part| 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19

Mean 16.452; Variance 46.284; scale 0.355 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1 53 100.0 10 16 R83096 HLA-B2702 CTL modulat 1. 88.7 125 1 P80289 Human VPre-B protein. 6. 88.7 142 1 P80289 V preB-Z protein. 6. 86.8 10 18 R95423 HLA-B2705.75-84. 6 86.8 10 18 R95423 HLA-B2705.75-84. 6 86.8 10 18 R3075 HLA-B2705.75-84. 6 86.8 17 13 R71425 Human HLA-B2702 CTL modulat 1 8 86.8 17 13 R71442 Human HLA-B270 CTL modulat 2 8 86.8 17 13 R71442 Human HLA-B270 CTL modulat 2 8 86.8 17 13 R71442 Human HLA-B27 (62-85) 8 17 13 R71443 Human MHC 1 alpha 1 d 8 86.8 17 13 R71444 Human MHC 1 alpha 1 d 8 86.8 17 13 R71444 Human MHC 1 alpha 1 d 8 86.8 17 13 R71444 Human MHC 1 alpha 1 d 8 86.8 17 13 R71444 Human MHC 1 alpha 1 d 8 86.8 24 13 R71434 Human MHC 1 alpha 1 d 8 86.8 24 13 R71434 Human MHC 1 alpha 1 d 8 86.8 24 13 R71434 Human MHC 1 alpha 1 d 8 86.8 24 13 R71435 Human MHC 1 alpha 1 d 8 86.8 24 13 R71435 Human MHC 1 alpha 1 d 8 86.8 24 13 R71435 Human MHC 1 alpha 1 d 8 86.8 24 13 R71435 Human MHC 1 alpha 1 d 8 86.8 25 18 R95417 HLA-B2705.60-84.	Result No.	Score	Query Match	Length	DB	Ð	Description	Pred. No.
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Human MHC 1 alpha 1 d MHC Class I-derived p Peptide fragment of H MHC-I peptide Dk-(61- HLA-B2702 CTL modulat Sequence of the human Sequence encoded by g xMEF2. Human MHC 1 alpha 1 d Aspergillus aculeatus Mutant insulin-stimul Insulin-stimulated pr ERR2. Cyclic-GMP stimulated 63 MC CAM PDE from cl HLA-B2702.75-84(D).	Alpha-helix of HLA-B HLA-B2702 CTL modulat HLA-B2702 84-79-84 pa HLA-B2702 CTL modulat HLA-B2702 CTL modulat HLA-B2702 CTL modulat HLA-B2702.60-84. HLA-B2702.60-84. Tumour associated 90K
21246674667466744	R95413 R83062 R95429 R95428 R92908 R95416 R95422 R93159
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### ALIGNMENTS

Example 14; Page 34; 80pp; English.

EXAMPLE 183085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MEC) antigens. This sequence corresponds to residues 75-84 of the alpha 1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient. 16-MAY.1996 (first entry)
HIA-B3702 CTL modulating peptide (B2702.75-84(L)).
Gyotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702. 12-0CT-1995.
05-APR-1995.
05-APR-1995.
05-APR-1995.
05-APR-1997.
06-APR-1997.
06-AP л R83096 standard; peptide; 10 AA. Synthetic. WO9526979-A1. RESULT 

Gaps ö Score 53; DB 16; Length 10; Pred. No. 1.30e+01; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative ; 9

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RESULT 2 ID P80289 standard; protein; 125 AA.

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PT Composis. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 11: 299P; English.

Example: Page 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-B2705.75-84.

HLA-B2705.75-84.

HLA-B2705.75-84.

HLA: p74; alphal-hellx; human-leucocyte-associated antigen; inhibitor; recal lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                         Nucleotide sequence selectively expressed in pre-B cells - used in probes for determining non-T acute lymphoblast leukaemia and for prepn. of polypeptide(s)

Disclosure; pp; English.

This is encoded by the genomic form of the variable region pre-B-1 sequence. The gene is not rearranged during pre-B cell development and is 4.6 kb upstream of the lambda-5 gene. This protein can associate with itself or with heavy chain V domains expressed in pre-B cells. Vpre-B-1 and lambda-5 form a complete V domain via non-covalent bonds. The gene is expressed only in pre-B cell lines. See also N80470-74, N80476-77 and N82441-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-1 protein.
cells; non-T acute lymphoblast leukaemia; ss;
                                                                                     01-JUN-1988.
27-NOV-1987; 117619.
27-NOV-1987; 6B-028433.
14-JUL-1987; GB-016497.
14-CCT-1987; GB-024100.
(HOFF) HOFFMANN-LA ROCHE AG.
BAUGE SR, KUGO A. Melchers GF, Sakaguchi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1995.
10-NOY-1994; U12985.
10-NOY-1993; US-150493.
(STRO ) UNIY LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T
R95423 standard; peptide; 10 AA.
R95423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 88.7%;
Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clayberger C, Kre WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                            N-PSDB; N80475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 rfllry 71
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WO9513288-A1.
07-DEC-1990
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1 RILLRY
                      V preB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                             Pre-B c
EP-2691
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This is encoded by the genomic form of the variable region pre-B-2
sequence. The gene is not rearranged during pre-B cell development.

This protein may associate with itself or with heavy chain V domains expressed in pre-B cells. The gene is expressed only in pre-B cells. The gene is expressed only in pre-B cells income and N80470-75, N80476-77 and N82442.
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Disclosure: pp: English:

This is encoded by the human pre-B gene which differs from the mouse pre-B-2 gene (of NB3441) at several posns. The gene is also selectively expressed in pre-B cell lines. Its pattern of expression follows that of Yper-B1 and lambda-5 in the mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence selectively expressed in pre-B cells - used in probes for determining non-T acute lymphoblast leukaemia and for prepn. of polypeptide(s)
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Pred. No. 6.38e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 1; Length 125;
Pred. No. 6.38e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V preB-2 protein.
Pre-B cells; non-T acute lymphoblast leukaemia.
EP-269127-A.
                 (first entry)
protein.
non-T acute lymphoblast leukaemia.
                                                                                                            01-JUN-1988.
27-NOV-1987; 117619.
27-NOV-1986; 6B-028433.
14-JUL-1987; GB-016497.
14-OCT-1987; GB-024100.
(HOFF ) HOFFMANN-LA ROCHE AG.
Bauer SR, Kudo A, Melchers GF, Sakaguchi N;
WPI: 88-148947/22.
N-PSDB; N80476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1988.
27-NOV-1987; 117619.
27-NOV-1986; GB-028433.
14-JUL-1987; GB-016497.
14-OCT-1987; GB-024100.
(HOFF) HOFFMANN'LA ROCHE AG.
WPI; 88-148947/22.
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ID P80288 standard; protein; 142 AA.
AC P80288;
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ID P83001 standard; protein; 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.7%;
ilarity 83.3%;
Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AA;
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                                             Human Vpre-B
Pre-B cells;
                                                                                             EP-269127-A.
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WO9505189-A.
23-FEB-1995.
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mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 10~\mathrm{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIA-B2702 CTL modulating peptide (B2702.75-84).

Yytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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R830661-R83085, R830960-R83096 and R93007-R92913 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequenc
corresponds to residues 75-84 of the alpha-1 domain of the class
                                                                                                                                                                                                                                                                                                                                    Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 R41212;
15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen: HLA: peptide: transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acceptance period of transplants from MHC unmatched - using Class I B75-84\ \mathrm{MHC} antigen of the recipient
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                                                 Length 10
                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide sequence is more commonly found within compounds of not more than 30 amino acids in length.
                                               Score 46; DB 18; I
Pred. No. 8.26e+01;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; DB 8; L
No. 8.26e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krensky AM, Parham P;
                                                                                                                                                                                                                                                                  16-SEP-1993.
25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1995.
05-ARR-1995; U04349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clayberger C, Krensky AM, Parham WPI; 95-358582/46.
Extension of acceptance period of
                                                                                                                                                        .r 6
R41212 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R83075 standard; peptide; 10 AA. R83075;
                                               86.8%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                    Clayberger CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996 (first entry)
                                                            Local Similarity
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1 RILLRY 6
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WO9526979-A1.
                                                                                                                                                                                                                                           Synthetic.
WO9317699-A.
                                                                                                                      1 RILLRY
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                                                 Query Match
Best Local 3
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I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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71424 F71418 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
were used to competitive inhibition the peptides diminish the
receptors. Via competitive inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplassias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-0cT-1995 (first entry)

Human MHC 1 alpha 1 domain peptide Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide Dk-(62-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
Goldstein A. Goodenow RS, Olsson L;
WP1: 95-098577/13.
Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell receptor;
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                                                                                                                                                                                                                                                                                                                                            Score 46; DB 16; Length 10;
Pred. No. 8.26e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 13; Length 17;
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R71442;
R71442;
L2-OCT-1995 (first entry)
Human HLA-B27-(62-85) antigen derived peptide.
Human HLA-B27-(62-85) antigen derived peptide;
interaction modulation; arthritis; neoplasias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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871425 standard; peptide; 17 AA.
871425;
12-0CT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                            86.8%;
llarity 83.3%;
Conservative
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83.3%;
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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Best Local Similarity
Matches 5; Conserv
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R71439-R71443 are human major histocompatibility complex class 1 (MFC 1) alpha 1 domain and HLA derived peptides and fusion peptides. They were used to modulate interactions between MFC 1/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment
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R71433;
12-0CT-1995 (first entry)
Human MHC 1 alpha 1 domain peptide [Ala85]-Dk-(69-85).
Major histoompatibility complex class 1; MHC 1; cell receptor;
Major histoompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide [Ala85]-Dk-(69-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.
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histocompatibility complex class 1; MHC 1; cell receptor;
1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 45; 103pp; English.
R71424-R71438 are human major histocompatibility complex class 1
RMC 1) alpha I domain derived peptides and peptide mutants, they were used to modulate interactions between MHC I and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
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Regulating cell surface receptor response - by modulating
interaction between MHC class I antigen and the cell surface
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                                                                                                                                                                                                                                                                                   Length 17;
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                                                                                                                                                                                            neoplasias, lupus erythematosus and arthritis quence 17 AA;
                                                                                                                                                                                                                                                                             Score 46; DB 13; I
Pred. No. 8.26e+01;
0; Mismatches 1;
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Pred. No. 8.26e+01;
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arthritis; neoplasias; lupus erythematosus
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                    Page 45; 103pp; English.
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871426 standard; peptide; 17 AA.
871426;
12-0CT-1995 (first entry)
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12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
Goldstein A, Goodenow RS, O
WPI; 95-098577/12.
                                                                                                                                                                                                                                                                             86.8%;
larity 83.3%;
Conservative
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83.3%;
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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WO9505189-A.
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Human [Phe74] HIA-B27-(62-85) antigen derived peptide.
Human [Phe74]-HIA-B27-(62-85) antigen derived peptide; cell receptor;
Human [Phe74]-HIA-B27-(63-85) antigen derived peptide; cell receptor;
Interaction modulation; arthritis; neoplasias; lupus erythematosus.
           Frample 4; Page 45; 103pp; English.
R71439-R71443 are human major histocompatibility complex class 1
(MRC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 45; 103pp; English.
R71439-R71443 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell
surface receptors. Via competitive inhibition the peptides diminish
the receptors response, this feature may be useful for the treatment
of neoplassas, lupus erythematosus and arthritis.
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Pred. No. 8.26e+01;
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Pred. No. 8.26e+01;
0; Mismatches 1;
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R71443 standard; peptide; 17 AA.
R71443;
12-0CT-1995 (first entry)
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R71440 standard; peptide; 17
R7440: 12-0CT-1995 (first entry)
                                                                                                                                                                                                                                                                             86.8%;
ilarity 83.3%;
Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
Goldstein A. Goodenow RS,
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Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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Best Local Similarity
Matches 5; Conserv
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WPI; 95-098577/
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WO9505189-A.
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Human MHC I alpha I domain peptide [Ala78]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor;

alpha I domain; peptide [Ala78]-Dk-(69-85); interaction modulation;

arthritis; neoplasias; lupus erythematosus.
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R7144-R71438 are human major histocompatibility complex class 1
R7144-R71438 are human major histocompatibility complex class 1
R7144-R71438 are human major histocompatibility manual competitive deptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
                          Example 4; Page 45; 103pp; English. R7144-R71438 are human major histocompatibility complex class 1 (MHC 1) alpha 1 domain derived peptides and peptide nutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment
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R71424.
12-071-1995 (first entry)
Human MHC 1 alpha 1 domain peptide Dk-(62-85).
Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide Dk-(62-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
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interaction between MHC class I antigen and the cell surface
                                                                                                                                                       Score 46; DB 13; Leuy...
Pred. No. 8.26e+01;
``.matches 1; Indels
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Pred, No. 8.26e+01;
                                                                                                                     of neoplasias, lupus erythematosus and arthritis
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R71428;
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Local Similarity 83.3%;
les 5; Conservative
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Similarity 83.3%;
5; Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
GOLdEtein A, Goodenow RS,
WPI; 95-098577/13.
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12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC.) UNIV CALIFORNIA.
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Best Local Similarity
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WPI, 95-098577/13
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WO9505189-A.
23-FEB-1995.
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WO9505189-A.
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Matches
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Gaps
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R71424-R71438 are human major histocompatibility complex class 1
R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplastas, lupus erythematosus and arthritis.
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Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Thu May 22 08:43:51 1997; MasPar time 1.74 Seconds 37.653 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-5 (1-6) from US08653294.pep 53

1 RILLRY 6 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

summaries Minimum Match 0% Listing first 45 summarie Maximum DB seq length 60 Post-processing:

Database:

a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Mean 16.452; Variance 46.284; scale 0.355 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	.30e+01	.26e+01	8.26e+01	.26e+01	.26e+01	.26e+01	.26e+01	26e+01		26e+01	26e+01 26e+01	26e+01 26e+01 26e+01	26e+01 26e+01 26e+01 26e+01						
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	tion	HLA-B2702 CTL modulat	HLA-B2705.75-84.	Peptide fragment of C	HLA-B2702 CTL modulat	Human MHC 1 alpha 1 d	Human HLA-B27-(62-85)	Human [Phe74]-HLA-B27	Human MHC 1 and HLA f	Human MHC 1 alpha 1 d		HUMAN MHC I ALDNA I O		MHC 1 705.60	MHC 1 2705.60					
	Ð	R83096	R95423	R41212	R83075	R71425	R71442	R71443	R71440	R71433	R71426	R71428	R71424	R71434	R71436	701170	7777	R71435	R/1435 R95417	K71435 R95417 R71420
	DB	16	18	æ	16	13	13	13	13	13	13	13	13	13	13	13	ì	13	13	13
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æ	Query Match	100.0	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8		86.8	86.8 86.8	86.8 86.8 86.8
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Peptide fragment of H MHC-I peptide Dk-(61- HLA-B2702 CTL modulat HLM-B2702.75-84(D). Alphal-helix of HLA-B HLA-B2702 CTL modulat HLA-B2702 84-79-84 pa HLA-B2702 84-79-84 pa HLA-B2702 CTL modulat HLA-B2702 CTL modulat HLA-B2702 CTL modulat HLA-B2702.60-84.
R41221 R69619 R83091 R71438 R95425 R95425 R95429 R95429 R95429 R95416 R95416
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Note: Post-processor removed 14 summaries from list due to search parameters chosen.

### ALIGNMENTS

RESULT	i fi
ü	R83096 standard: peptide: 10 AA.
AC A	,
DŢ	16-MAY-1996 (first entry)
DE	HLA-B2702 CTL modulating peptide (B2702.75-84(L)).
ΚW	Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
ΚW	immunosuppressant; graft versus host disorder; transplantation; therapy;
ΚW	class I MHC; HLA-B2702.
SO	Synthetic.
PN	WO9526979-A1.
PD	12-OCT-1995.
다	05-APR-1995; U04349.
PR	05-APR-1994; US-222851.
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.
ΡΙ	Clayberger C, Krensky AM, Parham P;
DR	WPI; 95-358582/46.
PŢ	Extension of acceptance period of transplants from MHC unmatched
ΡŢ	donor hosts - using Class I B75-84 MHC antigen of the recipient
ΡŢ	
PS	Example 14; Page 34; 80pp; English.
ខ	R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
ខ្ល	class I major histocompatibility complex (MHC) antigens. This sequence
ပ္ပ	corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
ပ္ပ	HLA-B2702. These sequences can be used to extend the period of
ပ္ပ	acceptance by a recipient of a transplant from an MHC unmatched donor.
ပ္ပ	The peptides are administered to a patient in conjunction with
ပ္ပ	a subtherapeutic amount of an immunosuppressant. This is administered to
ပ္ပ	the patient for a limited period of time (compared to the lifetime
ပ္ပ	administration for current treatments). The peptides particularly
ບ	
ပ္ပ	
SO	Sequence 10 AA;
õå	Query Match 100.0%; Score 53; DB 16; Length 10; Best Local Similarity 100 0%: Pred No 1 30e401.
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n 2 R95423 standard; peptide; 10 AA. RESULT
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Example 14; Page 34; 80pp; English.
R83061-R83085, R83090 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                       HIA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 45; 103pp; English.

R7144-R71438 are human major histocompatibility complex class 1

R7142-R71438 are human major histocompatibility complex class 1

(MHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
were used to ompetitive inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MHC 1 alpha 1 domain peptide Dk-(69-85).
Major histocompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide Dk-(62-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldstein A, Goodenow RS, Olsson L; WPI; 95-08677/13. Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 16; I
Pred. No. 8.26e+01;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                       (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R71425 standard; peptide; 17 AA. R71425;
                                                     standard; peptide; 10 AA.
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Similarity 83.3%;
5; Conservative
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1995 (first entry) Human MHC 1 alpha 1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                  12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
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Matches 5; Conser
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WPI; 95-358582/46.
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WO9505189-A.
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                                                                                                     16-MAY-1996
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                                                                             R83075;
                             R83075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               host
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                                                     셤
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                                                                                       Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

In Sequence represents the mannanian represents the mannanian represents the protein processor and receil lyates. PAGE as T-cell surface membrane protein processor and receil arth T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70. p74 is found in a limited number of cell types, but is particularly expressed on and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

Example of the possed for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis activity of T-cells, by combining the mount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing the binding of the p74 ligand.
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Wew peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL)

activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
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                                                                       Compsns. comprising lymphoid surface membrane proteins - which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide fragment of class, I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
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Pred. No. 8.26e+01;
0; Mismatches 1; Indels
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25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDERGER CA, Krensky AM;
WPI; 93-303134/38.
STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T
R41212 standard; peptide; 10 AA.
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Similarity 83.3%;
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Similarity 83.3%;
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                             Krensky AM;
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Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                       WPI; 95-194027/25.
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Regulating cell su
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WO9505189-A.
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Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.
Munan [Phe74]-HLA-B27-(62-85) antigen derived peptide; cell receptor; interaction modulation; arthritis; neoplasias; lupus erythematosus.
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R71439-R71443 are human major histocompatibility complex class 1 (MHZ 19. R714443 are human major histocompatibility complex class 1. They were used to medulate interactions between MHZ I/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
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R71439-R7143 are human major histocompatibility complex class 1
RMC139-R7143 are human major histocompatibility complex class 1
They were used to modulate interactions between MHC 1/HLA and cell
Surface receptors. Via competitive inhibition the peptides diminish
the receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
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Mana H.A. #827-(62-85) antigen derived peptide.
Human H.A. #827-(62-85) antigen derived peptide; cell receptor;
interaction modulation; arthritis; neoplasias; lupus erythematosus.
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WPI; 95-089577/13.
Regulating cell surface receptor response - by modulating
interaction between MHC class I antigen and the cell surface
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Pred. No. 8.26e+01;
0; Mismatches 1; Indels
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. 8.26e+01;
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Pred. No. 8.26e+01;
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ID R71442 standard; peptide; 17 AA.
AC R71442;
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R71443;
12-OCT-1995 (first entry)
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Local Similarity 83.3%;
les 5; Conservative
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WPI; 95-098577/13.
                           83.3%;
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12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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Matches 5; Conser
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RILLRY 6
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Best Local Similarity

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R71439-R71443 are human major histocompatibility complex class 1
RMC 1) alpha 1 domain and HAA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell
surface receptors. Via competitive inhibition the peptides diminish
the receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
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Human MHC 1 alpha 1 domain peptide (Ala85]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide (Ala85)-Dk-(69-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                             12-OCT-1995 (first entry)

Human MHC 1 and HLA fusion peptide HLA-A2-(69-76)DK-(77-85).

Human MHC 1 and HLA fusion peptide HLA-A2-(69-76)DK-(77-85).

Anjor histocompatibility complex class 1; MHC 1; cell receptor;

Alpha 1 domain; fusion peptide HLA-A2-(69-76)Dk-(77-85);

interaction modulation; arthritis; neoplasias; lupus erythematosus.
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R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
receptors. Via competitive inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
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Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
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8.26e+01;
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Pred. No. 8.26e+
0; Mismatches
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R71440 standard; peptide; 17 AA.
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R71433;
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.larity 83.3%;
Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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(REGC ) UNIV CALIFORNIA.
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R71434;
12-0CT-1995 (first entry)
Human MHC 1 alpha 1 domain peptide [Ala68, 75]-Dk-(62-85).
Major histocompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide [Ala68, 75]-Dk-(62-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.
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R71424-R71438 are human major histocompatibility complex class 1
R71424-R71438 are human major histocompatibility complex class 1
KMC 1) alpha I domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
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R71424-R71438 are human major histocompatibility complex class 1
R71426-R71438 are human major histocompatibility complex class 1
WHC 1) alpha 1 domain derived peptides and peptide mutants, they
were used to modulate interactions between MHC 1 and cell surface
receptors. Via competitive inhibition the peptides diminish the
receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                           12-0cT-1995 (first entry)

Human MHC 1 alpha 1 domain peptide Dk-(62-85).

Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide Dk-(62-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
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8.26e+01;
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Pred. No. 8.26e+01;
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R71424;
12-ocr-1995 (first entry)
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                                  86.8%;
|larity 83.3%;
|Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
                                                              Best Local Similarity
Matches 5; Conser
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WO9505189-A.
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                                                                 Gaps
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Human MHC 1 alpha 1 domain peptide [Ala71]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.
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Human MHC 1 alpha 1 domain peptide [Ala78]-Dk-(69-85).

Major histocompatibility complex class 1; MHC 1; cell receptor;
alpha 1 domain; peptide [Ala78]-Dk-(69-85); interaction modulation;
arthritis; neoplasias; lupus erythematosus.
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R71424-R71438 are human major histocompatibility complex class 1
R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplassas, lupus erythematosus and arthritis.
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Pred. No. 8.26e+01;
0; Mismatches 1; Indels
                                                              Indels
pred. No. 8.26e+01;
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                                                                                                                                                                                                                                                                                                 R71426 standard; peptide; 17 AA.
R71426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R71428 standard; peptide; 17 AA.
R71428;
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                               83.3%;
                                                                 Conservative
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
                               Best Local Similarity
Matches 5; Conser
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Matches 5; Conser
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WPI; 95-098577/13
                                                                                                                      11 rtllry 16
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RILLRY 6
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| RILLRY 6
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WO9505189-A.
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ID R71427 standard; peptide; 24 AA.

AC R71427

AC R71427

DE Human MHC 1 alpha 1 domain peptide [Ala74]-Dk-(62-85).

BE Human MHC 1 alpha 1 domain peptide [Ala74]-Dk-(62-85).

Whajor histocompatibility complex class 1; MHC 1; cell receptor;

KW Major histocompatibility complex class 1; MHC 1; cell receptor;

KW Major histocompatibility complex class 1; MHC 1; cell receptor;

KW Major 1995 across 1 lupus erythematosus.

NOSJ05189-A.

PN MOSJ05189-A.

PR 12-AUG-1994; U09189.

PR 12-AUG-1994; U09189.

PR 12-AUG-1995; US-105416.

PR (REGC ) UNIV CALIFORNIA.

PR (REGC ) UNIV CALIFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1995 (first entry)

Human MHC 1 alpha 1 domain peptide (Ala70, 771)-Dk-(62-85).

Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide (Ala70, 771-Dk-(62-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 45; 103pp; English. R71424-R71438 are human major histocompatibility complex class 1 (MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 13; Length 24;
Pred. No. 8.26e+01;
0; Mismatches 1; Indels
        Length 24;
                                                                            1; Indels
    Score 46; DB 13; ]
Pred. No. 8.26e+01;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                       RESULT 14

ID R1436 standard; peptide; 24 AA. AC. R71436 standard; peptide; 24 AA. DT 12-OCT-1995 (first entry)
DE Human MHC 1 alpha 1 domain peptide
KW Major histocompatibility complex C. MW arthritis; neoplasias; lupus erython S05 189-A. DT 12-NG-1994.

PD 22-FEB-1995.
PP 12-NG-1994; U09189.
PR 12-NG-1994; U09189.
PR 12-NG-1994; U08-105416.
PA (REGC) UNIV CALIFORNIA.
PA (REGC) UNIV CALIFORNIA.
PY (ADGASTEIN A) GOODGHOW RS, Olsson DR WIT; 95-098577/13.
PT Regulating cell surface receptor r interaction between MHC class I an PT interaction between MHC class I an CR (MHC 1) alpha 1 domain derived peptore used to modulate interactions CC receptors response, this feature m CC of neoplasias, lupus erythematosus SQ Sequence 24 AA;
86.8%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 86.8%;
Local Similarity 83.3%;
les 5; Conservative
Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                     18 rtllry 23
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Length 24;
                           Score 46; DB 13; Ler
Pred. No. 8.26e+01;
0; Mismatches 1;
                          Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
24 AA;
 Sequence
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φ 1 RILLRY Search completed: Thu May 22 08:44:00 1997 Job time: 9 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MasPar time 2.57 Seconds 66.443 Million cell updates/sec Thu May 22 08:42:00 1997; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

>US-08-653-294-4 (1-6) from US08653294.pep 49 Tabular output not generated.

Title:

Description: Perfect Score: Sequence:

1 RIALRY 6 PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir50 Database:

Mean 21.604; Variance 27.804; scale 0.777 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No Description esult Query No. Score Match Length DB ID Result

No matches found.

Search completed: Thu May 22 08:42:12 1997 Job time: 12 secs.

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- 12 march

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protein - protein database search, using Smith-Waterman algorithm Distribution rights by IntelliGenetics, Inc. MPsrch\_pp Thu May 22 08:41:35 1997; MasPar time 1.89 Seconds 67.442 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-4 (1-6) from US08653294.pep 49 1 RIALRY 6 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

59021 segs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 22.521; Variance 22.707; scale 0.992 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Result Query
No. Score Match Length DB ID

Pred. No.

No matches found.

Search completed: Thu May 22 08:41:43 1997 Job time : 8 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:42:30 1997; MasPar time 1.75 Seconds 37.295 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-4 (1-6) from US08653294.pep 49 Title: Description: Perfect Score:

1 RIALRY 6 Sequence: PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

a-geneseq26
l:partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Mean 15.638; Variance 39.027; scale 0.401

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

									X	(										
	Pred. No.	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01,	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	4.07e+01	9.64e+01	9.64e+01
	Description	Alphal-helix of HLA-B	HLA-B2702.75-84(D).	Peptide fragment of C	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 84-79-84 pa	HLA-B2702 CTL modulat	HLA-B2702 84-75-84 pa	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702.60-84.	HLAB38.6084.	HLA-B2702 CTL modulat	Peptide fragment of C	HLAB38 CTL modulating	Peptide fragment of H	PB145 serpin enzyme c	HLA-B2702.75-84(T).	HLA-B2702 CTL modulat
	ID	R95413	R95425	R41208	R83062	R83094	R95429	R92912	R95428	R92907	R92908	R95416	R95422	R83090	R41205	R83093	R48286	R92804	R95426	R83096
	DB	18	18	ω	16	16	18	16	18	16	16	18	18	16	œ	16	ω	18	78	16
	Query Match Length	10	10	10	10	10	12	15	20	20	20	25	25	25	25	25	25	43	10	10
æ,	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.8	85.7	85.7
	Score	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	45	42	42
i	Result No.	-	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	. 19

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ī			chosen.
9.64e+01	9.64e+01	HLA-B2702 CTL modulat 9.64e+01	Note: Post-processor removed 23 summaries from list due to search parameters choser
modulat	modulat	modulat	search
CTL	CIL	CIL	ě Ç
702	702	702	t du
4-B2	1-B2	4-B2	lis
HL	HL	HL	from
R83095	R92910	20 16 R92909	summaries
16	16	16	23
10	20	20	removed
85.7	85.7	85.7	essor
42	42	42	ost-proc
20	21	22	Note: Po

#### ALIGNMENTS

RES	
e e	R95413 standard; peptide; 10 AA.
4 E	NSD415; 12-NOV-1996 (first entry)
	Alphal-helix of HLA-B2702.
ΚW	HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
ΚW	T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
3	B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
X.	cytolysis; antigen presenting cell.
S C	Synthetic.
Z, f	. TO - 28 - 27 .
<u>g</u> 5	
4 C	10-NOV-11V44, ULAVOU.
4 0	
Id	nsky AM;
DR	WPI; 95-194027/25.
БŢ	Compsns. comprising lymphoid surface membrane proteins - which may
PŢ	inhibit cytolytic activity and differentiation of CTLs.
PS	Example; Page 11; 29pp; English.
႘	This sequence represents the alphal-helix of the
ပ္ပ	human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
႘	epitopes, and palindromes of it (such as R95428) can be used to isolate
ပ္ပ	the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
ပ္ပ	protein associated with T-cell activation in mammalian T-cells, and is
ប្ដ	also immunologically cross reactive with the heat shock protein Hsc70.
႘	p74 is found in a limited number of cell types, but is particularly
당	expressed on B and T cells. p74 can be isolated by lysis of a suitable
ខ	cell with an amphoteric detergent, and then passed through an affinity
ပ္ပ	column containing a covalently bound HIA-B2702 palindromic peptide.
ပ္ပ	Compositions comprising the extracellular fragment of p/4 combined with
3 8	HLA-BZ/UZ.00-064 (See M99410), Induces Calcium Inliux, and Inlibits
3 8	Cycocard I I wilders (Control of Cycotysis Canada of Cycotysis Canada of Cycotysis Canada of Control of Cycotysis of
3 5	Compounds for a soldered to the cytracellular activity of a complaint the activity of a complaint the activity of a complaint and a complaint a complaint and a complaint a complaint and a complaint and a complaint a compla
ָ נ	1-certs, by committing them with the extracertural potention of pit
ຍູຍ	<pre>determining the amount of binding between the candidate compound and p/4. Modulation of CTT. activity can be inhibited in a cellular composition</pre>
3 5	containing the college and antidon processing (above ) by adding the
ני ל	mix the extracellular portion of 774, in an amount sufficient to commote
ប្រ	with p74 for the binding of the p74 ligand.
SO	Sequence 10 AA; .
•	
ایس	Query Match 100.0%; Score 49; DB 18; Length 10;

Gaps ö Indels Pred. No. 1.25e+01; 0; Mismatches 0; Best Local Similarity 100.0%; Matches 6; Conservative

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5 rialry 10 ||||||| | RIALRY 6

d ò

2895425 standard; peptide; 10 AA.
R95425 standard; peptide; 10 AA.
R95425.
12-NOV-1996 (first entry)
HLA-B2702.75-84(D).
HLA-B2702.75-84(D).
HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell lysate; antigen presenting cell.
Synthetic.

RESULT
LD R9
AC R9
DT 12
DE H11
KW HI
KW B TKW B Cy
KW Cy
KW Cy
KW FT MAI
FT MI

Key Location/Qualifiers Misc\_difference 3 /note= "N3D mutation"

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Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                              Clayberger C, Krensky AM;

WPI: 95-194027/25.

WPI: 95-194027/25.

WPI: 95-194027/25.

WPI: 95-194027/25.

PT Compens. Comparising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

PS Example; Page 11; 29pp; English.

Example; Page 11; 29pp; English.

CC (11) These sequences can be used to isolate the protein contain a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc?O. P74 from a T-cell lysate. P74 is a T-cells, and is also immunologically cross reactive with the heat shock protein Hsc?O. P74 is a T-cell surface membrane protein associated with the heat shock protein Hsc?O. P74 is a T-cells. P74 can be isolated by lysis of a suitable cell with an emphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

CC Compositions compressing the extracellular fragment of P74 condidate compositions compressing the extracellular fragment of P74 and determining the amount of binding between the candidate compound and P74.

CC Compositions of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can
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The peptide is used to modulate cytocoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0;
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25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                               10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R41208 standard; peptide; 10 AA
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Claim 15; Page 9; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) Sequence 10 AA;
                                                                           HIA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
Immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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R83061-R83085, R83090-R83096 and R92007-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with
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                                                                                                                                                                                                                                                                                                                                                      Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.25e+01;
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W09556979-A1.
12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                           12-0CT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
R83062 standard; peptide; 10 AA.
R83062;
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R83094 standard; peptide; 10 AA.
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immunosuppressant; gra
class I MHC; HLA-B2702
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          than an anomal and a sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the than 19702 84-79-84 palindrome. These sequences can be used to isolate the protein passociated with T-cell activation in mammalian T-cells and is protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. The sequence of cell types, but is particularly expressed on B and T cells. P/A can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B3702 palindromic peptide. Compositions comprising the extracellular fragment of P/A combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolytic activity of compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate compound and p/A. Containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of P/A, in an amount sufficient to compete containing of the p/A, in an amount sufficient to compete containing the inhibited in a cellular composition of Services.
a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1996 (first entry)
HIA-B2702 84-79-84 palindrome.
HIA-B2702 84-79-84 palindrome.
HIA- p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: p74: alphal-helix; human-leucocyte-associated antigen; HSC70; APC;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
cytolysis; antigen presenting cell.
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HLA-B2702 CTL modulating peptide (B2702.70-84).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compsis. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example; Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
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                                                                                                                                                                              Score 49; DB 16; Length 10;
Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDETGER C, Krensky AM;
WPI; 95-194027/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; peptide; 12 AA.
                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                               10 AA;
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WO9513288-A1.
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Willy 35-1940/10.

Willy 35-1940/10.

Willy 35-1940/10.

Willy 35-1940/10.

Example, Page 12: 29pp; English.

Example, Page 13: 29pp; English.

Munan-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the His-B700 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cells, and is protein associated with T-cell lysate. P74 is a T-cells, and is protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70.

P74 is found in a limited number of cell types, but is particularly p74 is found in a limited number of cell types, but is particularly cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B7702 palindromic peptide.

Column containing a covalently bound HIA-B7702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HIA-B7702.60-84 (see R95416), induces calcium influx, and inhibites compounds and be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-B2702 194-75-84 palindrome.
TLA-B1 1941-1 helix; human-leucocyte-associated antigen; inhibitor;
T-Cell 1ysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calculum influx; cytcotoxic T lymphocyte; CTL; differentiation;
cytcjlysis; antigen presenting cell.
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graft versus host disorder; transplantation; therapy;
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Pred. No. 1.25e+01;
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10-NOV-1994, U12985.
10-NOV-1993, US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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05-APR-1994; US-222851
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using Class I B75-84 MHC antigen of the recipient

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donor hosts
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a bubtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA;
                                                                                                                                                                                                                       HIA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; the class I MHC; HLA-B2702.
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                                                            Score 49; DB 18; Length 20;
Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(S-TRD ) UNIV LELAND STANFORD JUNIOR.
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92907 standard; peptide; 20 AA.
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R92908 standard; peptide; 20 AA.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Local Similarity 100.0%;
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WPI; 95-358582/46.
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
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HLA-B2702.60-84.

HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;

T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
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Pred. No. 1.25e+01;
0; Mismatches 0; Indels
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Pred. No. 1.25e+01;
0; Mismatches 0;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytolysis; antigen presenting cell.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Local Similarity 100.0%;
6; Conservative
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R95416 standard; peptide;
R95416;
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WO9513288-A1.
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WO9526979-A1.
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Composes. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example Page 91, 29pp. English.

Example Page 91, 29pp. English.

CR95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the than R95415-R95431 represent palindromes and fragments of HLAB38 (6084. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated cuth T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein H8570. p74 is found in a constaining a covalently bound HLA-B2702 palindromic peptide.

Containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 compound and p74.

Cytotoxic T lymphocyte (CTL) differentiation or cytolytis. Candidate compounds can be screened for their effect on the cytolytic activity of determining them with the extracellular portion of p74 and determining the mount of binding between the candidate composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                              HLA-B2702 CTL modulating peptide (B2702.60-84). Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.25e+01;
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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85422; standard; peptide; 25 AA.
855422;
12-NOV-1996 (first entry)
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R83090;
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Best Local Similarity 100.0%;
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1 RIALRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Example 13; Page 32; 80pp; English.
R83061-R83085, R8309-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmarched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HIABS CTL modulating peptide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLAB38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CLL toxicity in transplantations, for inducing CLL activity in parasitic diseases and neoplashs and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 16; Length 25; Pred. No. 1.25e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1993.
25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STR) ) UNIV LELAND STANFORD JUNIOR.
CLAYDERGER CA, KRENSKY AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R41205 standard; peptide; 25 AA. R41205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA.
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Local Similarity 100.0%;
les 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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R83093 standard; peptide;
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05-APR-1995; U04349.
05-APR-1994; US-222851.
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Rample 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatability complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
(STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM, Parham P;
WPI: 95-35882/46.

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                           host
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ö Gaps ö Score 49; DB 16; Length 25; Pred. No. 1.25e+01; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 요

20 rialry 25 |||||| | RIALRY 6

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Search completed: Thu May 22 08:42:40 1997 Job time : 10 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:44:44 1997; MasPar time 2.46 Seconds 69.444 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-6 (1-6) from US08653294.pep 53 1 YRLLIR 6 Title:

Description: Perfect Score:

Sequence:

Scoring table:

89912 segs, 28507787 residues PAM 150 Gap 15 Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

pir50 Database:

Mean 22.841; Variance 31.665; scale 0.721 Statistics:

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Result Query
No. Score Match Length DB ID

Pred. No.

No matches found,

Search completed: Thu May 22 08:44:53 1997 Job time: 9 secs.

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Table .

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ATP-BINDING; NUCLEAR PROTEIN
                   SEQUENCE
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           BINDING
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Job time :
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                                                                                                                                                                                COLE K.P., BLAKELEY S.D., DENNIS D.T.;
PLANT PHYSIOL. 105:453-453(1994).
-!- FUNCTION: THIS PROTEIN BINDS RUBISCO SMALL AND LARGE SUBUNITS AND
-!- SUBUNIT: OLIGOMER OF PROBABLY SIX ALPHA AND SIX BETA SUBUNITS.
-!- SUBUNIT: OLIGOMER OF PROBABLY SIX ALPHA AND SIX BETA SUBUNITS.
-!- THIS PROTEIN SHOWS ATPASE ACTIVITY.
-!- SIMILARITY: BBLONGS TO THE CHAPERONIN (HSP60) FAMILY.
--- SIMILARITY: BBLONGS TO THE CHAPERONIN (HSP60) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DNA LIGASE IV (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)).
                                                                                                                                                                                                                                                          EMBL; Z272zz; creekeronins_CPN60.
PIR; S38642; S38642.
PROSITE; PS00296; CHAPERONINS_CPN60.
CHAPERONE; ATP-BINDING; CHLOROPLAST; TRANSIT PEPTIDE.
TRANSIT 1 45 CHLOROPLAST (BY SIMILARITY).
TRANSIT 46 583 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA.
61605 MW; 44188FDD CRC32;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                   01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA).
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                          EUKARYOTA; PLANTA; EKBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                   Score 55; DB 9; Length 583; Pred. No. 1.17e+01; 2; Mismatches 2; Indels
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                                                      PRT;
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232 ysliirrkplfy 243
           BRASSICA NAPUS (RAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN)
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                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                 TISSUE-SEED;
MEDLINE; 94302182.
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P49917;
                                                     RUB2_BRANA
P34794;
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SEGUENCE FROM N.A.
MEDLINE; 89174660.
JULY GALEAN J.W., LAWN R.M.;
J. BIOL. CHEM. 264:5957-5965(1989).
J. BIOL. CHEM. 264:5957-5965(1989).
J. BIOL. CHEM. 264:5957-5965(1989).
OF DIRONGYION: APO(A) IS THE MAIN CONSTITUENT OF LIPOPROTEIN(A). APO(A).
CAN BIND TO FIBRONECTIN AND HAS SERINE PROTEINASE ACTIVITY CAPABLE.
OF CLEAVING IT.
OF CLEAVING IT.
OF CLEAVING IT.
OF CLEAVING IS DISULFIDE LINKED TO APO-BIOO.
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-1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPEIN FAMILY.

EMBL; JO4635; G342073; --

FTR; A30848; A30848.

FTR; A30848; A30849; A2869.

FTR; A30848; A30848.

FTR;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MACACA MULATTA (RHESUS MACAQUE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
APOLIPOPROTEIN(A) (EC 3.4.21.-) (APO(A)) (LP(A)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 1; Length 1420;
Pred. No. 1.17e+01;
1; Mismatches 0; Indels
                                                                                                                                              Length 844;
                                                                                                                                                                                                                                         Indels
                                                                                                                                        Score 55; DB 3; Len
Pred. No. 1.17e+01;
3; Mismatches 2;
206 206 AMP (BY SIMILARITY).
844 AA; 96154 MW; A4C8599F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 1 1 2 SEQUENCE 1420 AA; 158367 MW; 03F1D517 CRC32;
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                                                                                                                                        Query Match 56.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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Similarity 85.7%;
6; Conservative
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RRIALRY 12
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CYTOPLASMIC.

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56.1%;
llarity 58.3%;
Conservative
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54565 M
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similarity 58.3%;
7; Conservative
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TISSUE-MUSCLE FIBROBLAST;
MEDLINE; 93345508.
                                                                                                                                                                                           STANDARD;
                                                                                                                            232 ysliirrkplfy 243
                                                                                                                                                 1 YRLAIRRIALRY 12
                                                                                             Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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491 AA;
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493 AA;
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ACHE_HUMAN
Q04844;
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CARBOHYD
SEQUENCE
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-1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE MUSCLE) OR CELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE MUSCLE) CHAINS.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY. EMBL, X02597; G57; --

ETR, X02597; G57; --

ERCEPTOR: POSISSINAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON EXTRACELLULAR.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: AFTER BINITING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 91377317.

RAD M.R., LUETZENKIRCHEN K., XU G., KLEINHANS U., HOLLENBERG C.P.;
YEAST 7:533-538 [1991.).

EMBL; X59720; E264423; -.

PIR; S19425, S19362.

PIR; S17476; S17476.

HYPOTHETICAL PROTEIN.

SEQUENCE 212 AA; 23590 MW; 35F0A90E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAKAI T., NODA M., MISHINA M., SHIMIZU S., FURUTANI Y., KAYANO T., IKEDA T., KUBO T., TAKAHASHI H., TAKAHASHI T., KUNO M., NUMA S.;
NATURE 315:761-764(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                             BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                      ö
                                                                       01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
HYPOTHETICAL 23.6 KD PROTEIN IN GLK1-STESO INTERGENIC REGION.
TCL34W OR YCL186.
SACCHAROWYCES CEREVISTAE (BAKER'S YEAST).
EUKARYOTA; FUNGI: ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                               Score 55; DB 11; Length 212;
Pred. No. 1.17e+01;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR.
                                                     212 AA
                                                                                                                                                                                                                                                                                                                                                                         491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                     ACHE_BOVIN STANDARD;
P02715;
21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                               / Match 56.1%;
Local Similarity 77.8%;
hes 7; Conservative
                                                     STANDARD;
  ||| |:|: : :
| YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 85240565.
                                                                                                                                                                                                                                                                                                          115 airrkvlry 123
                                                                                                                                                                                                                                                                                                                              4 AIRRIALRY 12
                                                    YCD4_YEAST
P25369;
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00236; NEUROTR ION CHANNEL.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
TRANSMEMBRANE; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON EXTRACELLULAR.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEESON D.M.W., BRYDSON M., BETTY M., JEREMIAH S., POVEY S., VINCENT A., NEWSOM-DAVIS J., EUR. J. BIOCHEM. 215:229-238(1993).

-!- FUNCTION: AFTER BINDING ACCTYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CORPORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE.

-!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BET DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR PESILON (IN MATURE MUSCLE) CHAINS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARIY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.

-!- DISEASE: THE MUSCLE ACHR IS THE MAJOR TARGET ANTIGEN IN THE AUTOIMMUNE DISEASE MYASTHENIA GRAVIS.

PENBL, X66403; G560153; --

PIR; S29601.

PIR; S29601.

PIR; S29601.

MIM; 100725; --

MIM; 100725; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                    ö
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                                                                                                                                               Score 55; DB 1; Length 491; Pred. No. 1.17e+01;
                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OL-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
OL-OCT-1996 (REL. 34, LAST SANNORATION UPDATE)
ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR.
                                                                       PROBABLE.
95EC2B5D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2BA86189 CRC32;
                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
POTENTIAL.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                           493 AA
                          BY SIMILARITY POTENTIAL.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (REL. 28, CREATED)
01-NOV-1995 (REL. 32, LAST SEQI
01-OCT-1996 (REL. 34, LAST ANN
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:44:16 1997; MasPar time 1.84 Seconds 69.215 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-6 (1-6) from US08653294.pep 53

Title: Description: Perfect Score: Sequence:

1 YRLLIR 6 PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 23.777; Variance 26.124; scale 0.910 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No. ü tesult Query
No. Score Match Length DB Result

No matches found.

Search completed: Thu May 22 08:44:25 1997 Job time: 9 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:46:31 1997; MasPar time 1.77 Seconds 36.872 Million cell updates/sec Run on:

Tabular output not generated

>US-08-653-294-7 (1-6) from US08653294.pep 49 Title:

Description: Perfect Score:

1 YRLAIR 6 PAM 150 Gap 15 Scoring table: Sednence:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 a-geneseq26 Database:

Mean 15.681; Variance 40.195; scale 0.390 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Pred. No.	-	1.52e+01	1.52e+01					4.80e+01	1.11e+02	1.11e+02
	Description	HLA-B2702 84-79-84 pa	HLA-B2702 84-75T/75-8	HLA-B2702 84-75-84 pa	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat	Drosophila-12 cadher	Protocadherin clone D	HLA-B2702 CTL modulat	HLA-B2702 CTL modulat
	ID	R95429	R95430	R95428	R92909	R92911	R92907	R58902	R87142	R92910	R92908
	DB	18	18		16	16	16	11	17		19
	Query Match Length DB	12	20	20	50	20	20	43	43	20	20
φ	Query	100.0	100.0	100.0	100.0	100.0	100.0	91.8	91.8	85.7	85.7
	Score	49	49	49	49	49	49	45	45	42	42
	Result No.	7	7	m	4	ഗ	9	7	ω	σ	10

Note: Post-processor removed 35 summaries from list due to search parameters chosen.

# ALIGNMENTS

LT 1 R95429 standard; peptide; 12 AA. R95429; RESULT ID R9 AC R9

PD 18-MAY-1995.

PP 10-NOV-1994; U1295.

PP 10-NOV-1994; U1295.

PR 10-NOV-1995; US-155APD 5TANFORD JUNIOR.

R (STRD) UNIV LELAND STANFORD JUNIOR.

PI (STRD) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM;

PT (STRD) UNIV LELAND STANFORD JUNIOR.

CCC (LAR-19-84 Pallinformer. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane to protein associated with T-cell activation in mammalian T-cells, and is a sultable compound in a limited number of cell types, but is particularly constructed to the passed through an affinity column containing a covalently bound HLA-B2702 pallindromic peptide.

CC (Compositions comprising the extracellular fragment of p74 and cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the with p74 for the binding of the p74 ligand.

Sequence 12 AA; 12-NOV-1996 (first entry)
HAAB2702 84-99-84 palinhame.
HIAA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
Cytolysis; antigen presenting cell.
W9513288-A1. 

Gaps ö Query Match 100.0%; Score 49; DB 18; Length 12; Best Local Similarity 100.0%; Pred. No. 1.52e+01; Matches 6; Conservative 0; Mismatches 0; Indels

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|||||| | YRLAIR 6

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12-NOV-1996 (first entry)
HIA-B2702 84-75g7/5-84r palindrome.
HIA-B2702 84-75g7/5-64r palindrome.
HIA-B2702 84-75g7/5-64r palindrome.
HIA-B2702 84-75g7/5-64r palindrome.
HIA-B704: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
Syptolysis; antigen presenting cell.
W09513288-A1. ¥. r R95430 standard; peptide; 20 R95430; A COUNTY OF THE PROPERTY OF TH

18-MAY-1995.
18-MAY-1995.
19-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1994; US-150493.
10-NOV-1994; US-15

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and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a sultable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human-leucocyte-associated antigans. This sequence represents the human-leucocyte-associated antigans. This sequence represents the HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate the protein py4 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell intrivation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly capressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity compositions comprising the extracellular fragment of F74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising the extracellular fragment of F74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits composition of CTL activity can be inhibited in a cellular compound and F74. And determining the amount of binding between the candidate compound and F74. Modulation of CTL activity can be inhibited in a cellular composition of mix the extracellular portion of F74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the containing the binding of the F74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 184-75-84 palindrome.
HLA-B2702 184-75-84 palindrome.
TLA-B1 lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytocxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example: Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 18; Length 20;
Pred. No. 1.52e+01;
0; Mismatches 0; Indels
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R95428 standard; peptide; 20 AA.
R95428;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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| YRLAIR 6
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Matches
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75.84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                               HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immnosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                         Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 16; Length 20;
Pred. No. 1.52e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Krensky AM, Parham P;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                               20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R92911 standard; peptide; 20 AA.
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Local Similarity 100.0%;
les 6; Conservative
                                                                                                                                  (first entry)
                                                                                           standard; peptide;
                                                                                                                                                                                                                                                                                                 US-222851
                                                                                                                                                                                                                                                            12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1995; U04349
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WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C,
                                                                                                                                                                                                                                          WO9526979-A1.
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1 YRLAIR 6
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YRLAIR
                                                                                                                              16-MAY-1996
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                                                                         R92909;
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Polymorlectide(s) encoding human protocadherins pc3 and pc4 and rat pc5 involved in cell-cell adhesion and regulation activities Example 2; Page 67-68; 146pp; English.

R87142-R87144 represent partial fragments of the drosophila protocadherin sequence. The cDNAs encoding these sequences were isolated after screening a drosophila whole body cDNA preparation with the primers shown in 103575 and 103576. The primers were constructed from portions of the amino acid sequences of the third and fourth extracellular domains of
      For modulating natural binding and regulating activities.

Example: Page 63: 114pp; English.

Two regions of conserved AA sequence, one from the middle of the Two regions of conserved AA sequence, one from the other from the C.C. third cadherin extracellular subdomain (EC-4) were identified. The corresp. degenerate oligos (06694), 068950) were designed for use as PCR primers. PCR was carried out on a rat brain cDMA prepn. Two major bands of about 450 bps and 130 bps were found. The 450 bp and corresponded to the expected length between the two primer sites, but the 130 bp band could not be predicted from any of the previously identified cadherin sequences. The 450 bp and 130 bp bands were extracted and sequenced. Nineteen novel partial cDNA clones were isolated. The DNA and deduced AA sequences of the clones were isolated. The DNA and deduced AA sequences of the clones (including sequences corresp. to the PCR primers) are given in 068911.06896994 and R5880-ES8878. Various cDNA fragments conse and xenopus brain cDNA prepns. by PCR using the above primers. The DNA and deduced AA sequences of the resulting PCR fragments corresp. To the PCR primers.

The DNA and deduced AA sequences indicates a similarity in particular, the deduced AA sequences indicates a similarity, in particular, of the deduced AA sequences indicates a similarity, in particular, there are three sets of clones that appear to be cross-species homologues: RAT-218, MOUSE-322 and HUMAN-11; RAT-314, MOUSE-321 and HUMAN-11; AAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1996 (first entry)
Protocadherin clone DROSOPHILA-12.
Protocadherin; pa3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly.
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 11; Length 43;
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0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.8%;
83.3%;
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39
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Misc_difference 40
/note= "encoded by ACA"
Misc_difference 41
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Misc_difference 42
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Misc_difference 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by CGC"
WO9600289-A1.
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Best Local Similarity
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26-JUN-1995; U08071.
27-JUN-1994; US-2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 96-068873/07.
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Misc_difference
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29-AUG-1996
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (Comparad to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY.1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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05-APR-1995; U04349.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STB) 1UNI LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358882/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using class I B75-84 MHC antigen of the recipient
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N-PSDB; Q68993.
Polynucleotide sequences encoding new proto:cadherins - useful
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17-APR-1995 (first entry)
Drosophila-12 cadherin-related molecule.
Cadherin; cell adhesion molecule.
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                     standard; peptide; 20 AA.
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 6; Conservative
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23-DEC-1993; U12588.
29-DEC-1992; US-998003.
                                                                                                      20 AA:
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| YRLAIR 6
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WO9526979-A1.
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WO9414960-A.
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published cadherin sequences. The cytoplasmic domain of cadherin interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cell-call adhesion. These sequences may have regulatory functions in the cell, as well as the cell-call adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92307-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILs)
                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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WHI; 95-388882/46.
WHI; 95-38882/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 4.80e+01;
0; Mismatches 1; Indels
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Pred. No. 1.11e+02;
0; Mismatches 1; Indels
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                              JT 9
R92910 standard; peptide; 20 AA.
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R92908 standard; peptide; 20 AA.
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llarity 83.3%;
Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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WO9526979-A1.
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Example 15; Page 36; 80pp; English.

Example 15; Page 36; 80pp; English.

Example 15; R83096-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MRC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of complex complex from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate for unmints). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.11e+02;
0; Mismatches 1; Indels
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12-OCT-1995.
05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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1larity 83.3%;
Conservative
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US-08-653-294-7.rpr

***************************************	**************************************	Distribution rights by IntelliGenetics, Inc. MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Run on: Thu May 22 08:46:03 1997; MasPar time 2.50 Seconds	b8.363 Million cell updates/sec Tabular output not generated.	
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>US-08-653-294-7 (1-6) from US08653294.pep 49 1 YRLAIR 6 PAM 150 Gap 15 Title: Description: Perfect Score: Sequence: Scoring table:

89912 seqs, 28507787 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev Mean 21.577; Variance 27.148; scale 0.795 Statistics:

SUMMARIES

Result Query No. Score Match Length DB ID Description Pred. No.

No matches found.

Search completed: Thu May 22 08:46:13 1997 Job time: 10 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:32:13 1997; MasPar time 1.92 Seconds 33.977 Million cell updates/sec Run on:

not generated Tabular output

(1-6) from US08653294.pep >US-08-653-294-7 Description: Perfect Score: Sequence: Title:

1 YRLAIR 6

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 a-geneseq26 Database:

Mean 15.681; Variance 40.195; scale 0.390 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMÁRIES

Result No.	Score	Query	Query Match Length DB	DB	Ω	Description	Pred. No.
. ⊢	4.9	100.0	12	18	R95429	HLA-B2702 84-79-84 pa	1.52e+01
7	49	100.0	20	8	R95430	84-75T/75	1.52e+01
m	49	100.0	20	18	R95428		1.52e+01
4	49	100.0	20	16	R92909	CIL modul	1.52e+01
5	49	100.0	20	16	R92911	HLA-B2702 CTL modulat	1.52e+01
9	49	100.0	20	16	R92907	HLA-B2702 CTL modulat	1.52e+01
7	45	91.8	43	11	R58902	Drosophila-12 cadher	4.80e+01
80	45	91.8	43	17	R87142	Protocadherin clone D	4.80e+01
σ	44	89.8	724	18	R93081	Bacillus thuringiensi	6.37e+01
10	44	89.8	772	15	R79949	Enzyme M-11.	6.37e+01
11	44	8.68	775	15	R79950	Enzyme 036.	6.37e+01
12	42	85.7	20	16	R92910	HLA-B2702 CTL modulat	1.11e+02
13	42	85.7	20	16	R92908	HLA-B2702 CTL modulat	1.11e+02
14	41	83.7	617	ω	R42392	McI haemagglutinin.	1.47e+02
15	41	83.7	732	~	R11056	Acylamino acid-isolat	1.47e+02
16	41	83.7	732	m	R20001	Human acyl amino acid	1.47e+02
17	41	83.7	783	13	R70841	E. coli polymerase-II	1.47e+02
18	41	83.7	783	'n	R24441	E. coll DNA polymeras	1.47e+02
19	41	83.7	783	Н	P94265	Seguence of APH36.1 c	1.47e+02
20	40	81.6	232	<del>, -1</del>	P80760	Deduced peptide seque	1.93e + 02

6.6	ກຸດກຸ	1.93e+02	٠, ٠	2.53e+02	u )	u)	٠:	٠:	n;	ď	2	2	ä	u)	u)	ū	'n	2.53e+02	2.53e+02	2.53e+02	3.31e+02
32 kd alveolar ine 32K alveola	ィャ	Insecticidal protoxin	¥	seata Baci veloprolife	MPLV env protein with	thuring	67-kD protein toxin.	Retinoblastoma 94kD t	Human retinoblastoma	Human retinoblastoma	Cancer supressing gen	Retinoblastoma pplioR	Retinoblastoma tumour	Predicted retinoblast	(RB)	Recombinant pp110RB p	stoma	Mouse DEC-205.	Human DEC-205.	eryA region polypepti	G-protein coupled hum
P60437 R04210	R29815 R05591	R48678	0 0	R75940	R23970			99	R58568	P82112	30	88	$\sim$	628	R36534	R71681	P90599	W00645	W00644	R44430	W02699
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44	4.4	40	0 0	6 8 8	39	39	39	39	39	39	33	33	39	33	36	36	33	39	36	39	38
222																					45

## ALIGNMENTS

12-NOV-1996 (first entry)
HIA-B3702 84-79-84 palindrome.
HIA-B3702 84-79-84 palindrome.
HIA-B3702 84-79-84 palindrome.
HIA-P4-84 palindrome.
HIA-P4-84 superior helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
Syptolysis; antigen presenting cell.
WQ9512288-A1. 18-MAY-1995. 10-NOV-1994; U12985. 10-NOV-1993; US-150493. (STRD ) UNIV LELAND STANFORD JUNIOR. Clayberger C, Krensky AM; WPI; 95-194027/25. T R95429 standard; peptide; 12 AA. 

Score 49; DB 18; Length 12; Pred. No. 1.52e+01; Query Match Best Local Similarity 100.0%;

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Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1995; U04349
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WPI; 95-358582/46.
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HIA-B2702 84-75T/75-84T palindrome.
HIA-B2702 84-75T/75-84T palindrome.
HIA- p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA- p74; alphal-helix; human-leucocyte-associated strongen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
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HIA-B2702 84-75-84 palindrome.
HIA: p74; alphal.helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytocxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
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   Gaps
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Pred. No. 1.52e+01;
0; Mismatches 0; Indels
   Indels
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0
   Mismatches
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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10-NOV-1994.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R95430 standard; peptide; 20 AA.
R95430;
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Clayberger C, Krensky AM;
WPI; 95-194027/25
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 Conservative
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| YRLAIR 6
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for unrent treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).

Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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Compons. comprising lymphoid surface membrane proteins - which inhibit cytolytic activity and differentiation of CTLs. Example; Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments
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Pred. No. 1.52e+01;
0; Mismatches 0
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Pred. No. 1.52e+01
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92909 standard; peptide; 20 AA.
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Best Local Similarity 100.0%;
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Matches 6; Conservative
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07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003.
(DOHE-) DOHENY EYE INST.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a
                                                                                                 16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                            Example 15; Page 36; 80pp; English.

Example 15; Ras090-Ras096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
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WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 1.52e+01;
"...matches 0; Indels
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P
WPI; 95-356582/46.
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                           standard; peptide; 20 AA.
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WO9526979-A1.
                 1 YRLAIR
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Best Local S
Matches
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R92907 S
R92907;
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R92911
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Occurs Watch

Matches 6; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 6; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 6; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 6; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; daps 0; 1 yeldes 0; Conservative 0; Mismatches 0; Indels 0; Mismatches 0; Mismatches 0; I
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Gaps

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1; Indels

Mismatches

Length 724;

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Claim 17; Fig 5; 55pp; French.

The present sequence is that of the JEG80 protein which was isolated from Bacillus thuringlensis ser. Jegathesan 37; [8149367], it is a crystal toxin of mol. wt. 80 kD which is active against dipteran insects, esp. mosquitoes. The full-length, recombinant JEG80 toxin, had mean LG50 values (in ng/ml) after 48 hours of 18.8, 42.7 and 10.1 against larvae of Aedes aegypti. Anopheles stephensi and Culex pipiens, respectively Wild-type Bijeg367 crystals gave values of 47.4, 54.5 and 9.6. The Mosquito Species tested) than the Bt CryIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference 502..506
/note= "used for production of probe sequence (T04206)"
Misc_difference 621..625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "used for production of probe sequence (T04207)"
EP-674005-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose; amylaceous saccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 18; Pred. No. 6.37e+01;
                                                                                                                                                                                                                                                                                                                                 toxin, despite their close sequence similarity Sequence 724 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1995; 301176.
23-FEB-1994; JP-047956.
23-FEB-1994; JP-047956.
26-APR-1994; JP-090728.
06-APR-1994; JP-090705.
(HAXE) HAXARAHIBARA SETBUTSU KAGAKU.
White MAXEMENT & Sugimoto T, Tsusaki K; WPI: 95-329870/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R79949 standard; Protein; 772 AA. R79949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%;
llarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          89.8%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1996 (first entry)
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium sp. M11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzyme M-11
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                NEW TOOLS OF THE PRESENT OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities

Example 2, Page 67-68, 146pp; English.

Example 2, Page 67-68, 146pp; English.

ERSIA12-RR144 represent partial fragments of the drosophila protocadherin sequence.

ERSIA12-RR144 represent partial fragments of the drosophila protocadherin sequence.

The cDNAS encoding these sequences were isolated after soremening a drosophila whole body cDNA preparation with the primers shown in TO3575 and TO3576. The primers were constructed from portions of the amino acid sequences of the third and fourth extracellular domains of the camino acid sequences of the third and fourth extracellular domains of the published cadherin sequences. The cytoplasmic domain of cadherin and construction through catenins and other cytoskeleton cascociated proteins. The cytoplasmic domain is not present in all cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in coll-cell adhesion. These sequences may have regularory functions in the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of construction of these protocadherins, and can be used therapeutically.
      Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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04-0CT-1996 (first entry)
accillus thuringlensis insecticidal protein JEG80.
Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae;
Aedes aegypti; Anophers stephensi; Culex pipiens; Btjeg 367.
Bacillus thuringiensis ser. jegathesan 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New B.thuringlensis ser. jegathesan insecticidal proteins - and related DNA, with high activity against dipteran larvae, e.g. A.aegypti, A.stephensi or C.pipiens
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                                                                                                   Location/Qualifiers
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R93081 standard; Protein; 724 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.8%;
Best Local Similarity 83.3%;
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24-AUG-1995; F01116.
25-AUG-1994; FR-010299.
(INSP ) INST PASTEUR.
Deleciuse A, Thiery I;
WPI: 96-151374/15.
N-PSDB; T17044.
                                                                                                                                                                                                                                                                                                                       Misc_difference 41
/note= "encoded by ATG"
Misc_difference 42
/note= "encoded by CGC"
Misc_difference 43
                                                                                                                                                                                                                                                                                         encoded by ACA"
ference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOHE-) DOHENY EYE INST
                                                                     Orosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "encoded by CGC"
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27-JUN-1994; US-268161.
                                                                                                                                                               /note= "encoded by C
Misc_difference 39
/note= "encoded by A
Misc_difference 40
                                                                                                                                    Misc difference 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 96-068873/07.
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WO9600289-A1.
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DNA encoding enzyme reduces amylaceous saccharide to produce non-reducing sugar with trehalose end gp. - useful in foods, Cosmetics, pharmaceuticals, etc.

PT cosmetics, pharmaceuticals, etc.

Claim 3: Page 21-22: 178pp; English.

Claim 3: Page 21-22: 178pp; English.

Claim 3: Page 21-22: 178pp; English.

CC This sequence represents an enzyme that forms a non-reducing sugar with a trehalose end group, from a reducing amylaceous saccharide. The amylaceous saccharides are a degree of glucose polymerisation of 3 or higher. This sequence was extracted from a liquid culture of Rhizobium species M-11. By using an oligonucleotide probe based on a fragment of this sequence, the encoding sequence was obtained. The encoding sequence was then ligated into a vector and used to produce M-11 in E.coli transformants. This can also be performed for the DNA encoding enzyme compact of the superstand for the buse of the color of the second adjuvants. The sugars can also be used as intermediates for the holose. The advantages with using these sugars, are that, they are the advantages with using these sugars, are that, they are practically non-reducing (so no browning reaction occurs when they are heated with proteins), have a mild but good quality sweetness, adequate viscosity and moisture-retaining properties.
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)5-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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| YRLAIR (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NN encoding enzyme reduces amylaceous saccharide to produce non-reducing sugar with trehalose end gp. - useful in foods, cosmetics, pharmaceuticals, etc.

To sametics, pharmaceuticals, etc.

Claim 3; Page 23-25; 178pp; English.

Claim 3; Page 20-25; 178pp; English.

This sequence represents an enzyme that forms a non-reducing sugar with a creaming group, from a reducing amylaceous saccharide. The anylaceous saccharides have a degree of glucose polymerisation of 3 or higher. This sequence was extracted from a liquid culture of the enzyme sequence of glucose polymerisation of 3 or higher. This sequence was then ligated into a vector and used to produce the encoding sequence was then ligated into a vector and used to produce the encoding sequence was then ligated into a vector and used to produce the encoding enzyme M-11 (see TO4155), which was obtained from Rhizobium sp. CC an be used in foods, cosmetics, pharmaceuticals and feeds. They are come used in foods, cosmetics, pharmaceuticals and feeds. They are sugars produced by the action of these enzymes come used an adjuvants. The sugars can also be used as intermediates to retribatose. The advantages with using these sugars, are that, they are practically non-reducing (so no browning reaction occurs when they care heated with proteins), have a mild but good quality sweetness, consider and adjuvente-retaining properties.
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HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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Pred. No. 6.37e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference 120..125
/note="used for production of probe sequence (T04209)"
Misc_difference 621..625
/note="used for production of probe sequence (T04210)"
EP-674005-A2.
                                                                                                                                                                                                                                                                                      Enzyme 036.
Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1995; 301176.
23-FEB-1994; JP-047956.
23-FEB-1994; JP-047940.
06-APR-1994; JP-0907028.
(HANYB) HAYARAHIBARA SEIBUTSU KAGAKU.
WPI; 95-329870/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Kev Location/Qualifiers
                                                                                                                                                                                      R79950 standard; Protein; 775 AA.
R79950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R92910 standard; peptide; 20 AA. R92910;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                        24-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                        amylaceous saccharide.
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05-APR-1995; U04349.
8 yrlqir 13
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                                    1 YRLAIR
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Example 15; Page 36; 80pp; English.

R8306-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (WHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate for unministered to the compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R93907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HAA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subcharapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immnosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Clayberger C, Krensky Aw, russers Clayberger C, Krensky Aw, russers Clayberger C, Krensky Aw, russers Carbon of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 16; Length 20;
Pred. No. 1.11e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 16; Length 20;
Pred. No. 1.11e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clavberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .T 13
R92908 standard; peptide; 20 AA.
R92908;
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llarity 83.3%;
Conservative
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larity 83.3%;
Conservative
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                                                                                                                                                                                                                                                                                Claim 11; Page 47-50; 119pp; English.

HA (051088-94) and fusion glycoprotein (051095-97) sequences of several wild-type measles strains are given. Shared amino acid variations in wild-type measles glycoproteins are identified in five wild-type measles viruses. A consensus polypeptide, the amino acid sequence of which reflects variation common to more than one wild-type strain, is the basis for constructing live attenuated vaccines, or recombinant vaccines to replace older, less efficacious vaccines. Immunological reagents useful in differentiating wild-type measles strains from other known strains can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic engineering.
Claim 1; Fig 2; 10pp; Japanese.
The sequence was obtd. from asix clones isolated from a pig liyer cDNA library. The clones, lambda AARE 419, 450, 451, 452, 521 and 522 cover the entire sequence of the gene.
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29-JUN-1989; 165216.
29-JUN-1989; JP-165216.
29-JUN-1989; JP-165216.
WPI, 91-084340/12.
N-PSDB; Q10958.
Acylamino acid-isolating enzyme-like polypeptide - prepd. by
                                                                                                                                                                                                                                       Haemagglutinin and fusion glycoprotein of several wild-type measles strains - used to construct vaccines for measles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 8; Length 617;
Pred. No. 1.47e+02;
2; Mismatches 0; Indels
                           13-MAY-1994 (first entry)
MCI haemagglutinin.
HA: fusion glycoprotein; wild-type;
measles virus; vaccine; infection; consensus polypeptide.
Measles virus strain MCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 732;
Pred. No. 1.47e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MXY-1991 (first entry)
Acylamino acid-isolating enzyme-like polypeptide.
AARE; pig liver.
                                                                                                                           28-CCT-1993

08-APR-1993; U03209.

08-APR-1992; US-866033.

(USSH ) US DEPT HEALTH & HUMAN SERVICE.

Bellini WJ. Rota JS;

WPI: 93-351735/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 15
R11056 standard; Protein; 732 AA.
R42392 standard; Protein; 617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7% nes 4; Conservative
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J03030673-A.
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Search completed: Thu May 22 08:32:26 1997 Job time: 13 secs.

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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

C -!- SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SIMILARITY TO HELICASES OF THE SNF2/RAD54 FAMILY.

EMBL; Z48618; G728695; -.

R EMBL; Z72672; E24354; -.

W HYPOTHETICAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HELICASE; PYPOTHETICAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HELICASE; DOMAIN 259 268 POLY-ALA.

T DOMAIN 259 268 POLY-GLU.

T DOMAIN 568 573 POLY-GLU.

T DOMAIN 675 682 POLY-GLU.

T DOMAIN 675 682 POLY-GLU.

T NP\_BIND 731 738 ATP (POTENTIAL). ANTHRANILATE SYNTHASE
NITROSOGUANDINE RESI
HYPOTHETICAL 65.5 KD
GLUCOSE INHIBITED DIV
KINESIN HEAVY CHAIN.
GRRI PROTEIN.
ADENILATE CYCLASE (EC
SIGNAL RECOGNITION PA
HYPOTHETICAL 21.2 KD
HYPOTHETICAL 26.6 KD
PHYPOTHETICAL 26.6 KD
PHYDROXYBENZOATE HYD
PHYDROXYBENZOATE HYD
POTROXYBENZOATE HYD
PROXYBENZOATE HYD
PROXYBENZOATE HYD
PROTEASE LA HOWOLOG (
HYPOTHETICAL 84.6 KD
MITOCHONDRIAL RESPIRA 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 171.5 KD HELICASE IN LYS5-ARO2 INTERGENIC REGION.
YGL150C OR G1880.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES. HYPOTHETICAL 29.3 KD 60S RIBOSOMAL PROTEIN 60S RIBOSOMAL PROTEIN DYNEIN HEAVY CHAIN, C GLUCOSYLTRANSFERASE-I GLUCOSYLTRANSFERASE-I PROTEASOME COMPONENT POLY-ALA.
POLY-GLU.
POLY-SER.
POLY-GLU.
POLY-GLU.
ATP (POTENTIAL).
ATB (POTENTIAL).
MW; 8149887E CRC32; PRT; 1489 AA PRC3\_XENLA TDF2\_SCHPO RL1\_YEAST TRPE\_BUCAP SNG1\_YEAST YKTA\_CAEEL GIDA\_ECOLI GIDA\_ECOLI GRR1\_YEAST YIAC\_HAEIN YIAC\_HAEIN YIAC\_HAEIN YIAC\_HAEIN YX31\_MYCTU RCA1\_YEAST CONLI PHHY\_PSEELE PHHY ALIGNMENTS SEQUENCE FROM N.A. MEDLINE; 96128061. JAMES C.M., INGE K.J., OLIVER S.G., YEAST 11:1413-1419(1995). 

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CREATED)

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SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE; 95400292.
MURARAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
SASANUWA S.-I., SASANUWA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
YAMAZAKI M., TASHIRO H., EKI T.;
YAMAZAKI M., 10.261-268(1995).
EWBI: D50617; 8336763; -.
                                                                                        01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SNOWDATION UPDATE)
HYPOTHETICAL 25.9 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.5 KD PROTEIN IN NAUS-HOM6 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
ROSE M., KORTER P., ENTIAN K.D.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENEL: Z4655; G1015872; -..
HYPOTHETICAL PROTEIN.
SEQUENCE 239 AA; 27567 MW; OBF23C6E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (FFIIB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 11; Le
Pred. No. 4.88e+00;
1; Mismatches 0;
                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YJR135C OR J2122.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 11;
Pred. No. 4.88e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 221 AA; 25915 MW; 3D34764A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULFOLOBUS SHIBATAE,
ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES.
[1]
                                                         221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%;
llarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Best Local Similarity
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1 YRLLIR 6
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| YRLLIR 6
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YJ9D_XEAST
P47167;
                                     LT 6
TF2B_SULSH
P50387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                       STRAIN-S286C / AB972;
DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R., AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M. CHUNG E., BERNO A., GUZHAN E., HARTZELL G., HUNICKE-SMITH S., HYMAN R., KAYSER A., KOWP C., LASHKARI D., LEW H., LIN D., MOSEDALE D., NAKAHARA K., NAMATH A., NORCREN R., OSENER P., OH C., TAYLOR P., WEI Y., YELTON M., SCHRAMM S., SHOGREN T., SMITH V., SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 94129084.
MIYAKE S., OKISHIO N., SAMEJIMA I., HIRAOKA Y., TODA T., SALTOH I.,
YANAGIDA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE MCM2/3/5 FAMILY.
EMBL; S68467; G545211; -.
EMBL; Z69369: E221200; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL 12.2 KD PROTEIN IN MMS21-UBC8 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 11; Length 101;
Pred. No. 2.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 6; Length 720;
Pred. No. 2.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Zb93c9; Leg 188723.

PIR; A48723; A48723.

PROSITE; PSO0847; MCM235.

TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;

DNA REPLICATION; CELL CYCLE; ATP-BINDING.

312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
A -> R (IN REF. 1).
29D61458 CRC32;
                                                 YELOTIC.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDA4 OR SPACJFIO.01.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKRRYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                           101 AA; 12209 MW; BE5A484B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (REL. 32, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CELL DIVISION CONTROL PROTEIN NDA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOL. BIOL. CELL 4:1003-1015(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 72-720 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            92.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 4
720 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 yrmlir 97
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| YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 3
NDA4_SCHPO
P41389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
NP_BIND
CONFLICT
SEQUENCE
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FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAYAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS I., HEDBLOM E., COTTON M.D., UTTENBACK T.K., HANNA M.C., NGUYEN D.T., SADUDK D.M., BRANDON R.C., EINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLITZ O. KRAH M., BORRIESS R.;
POLITZ O. KRAH M., BORRIESS R.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CALALYITC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-BETA-D-
LINKAGES IN MANNANS, GALACTOMANNANS, GLUCOMANNANS, AND
GALACTOGLUCOMANNANS.
-!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
EMBL, X90947; G9757065.
HYDROLASE; GLYCOSIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 95024047.
WAKASUGI T., ISUDZUKI J., ITO S., NAKASHIMA K., ISUDZUKI T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 6; Length 968;
Pred. No. 4.88e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
NONPHOTOSYNTHETIC, NONFRUITING GLIDING; CYTOPHAGACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPOB.
PINUS THUNBERGII (GREEN PINE) (JAPANESE BLACK PINE)
                                                                                                                                                                                                                                                 CHUCKOFLASI:
EUKARYOTA; PLANTA; EMBRYOPHYTA; CONIFEROPHYCEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 4; L
Pred. No. 4.88e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110219 MW; 0EA79E71 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANA_RHOMR STANDARD; PRT; 968 AA.
P49425;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78)
                                                                                                                                                                                                                                                                                                                                                                              629 AA; 70103 MW; 6FD83D06 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1075 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.6%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 5; Conser
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1 YRLLIR 6
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1 YRLLIR
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                                                                                                                                                                                                                                 VENTER J.C
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                      Score 48; DB 9; Length 303; Pred. No. 4.88e+00; ****matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 4; Length 628;
Pred. No. 4.88e+00;
1; Mismatches 0; Indels
                  MEDLINE, 95320218.
QURESHI S.A., KHOO B., BAUMANN P., JACKSON S.P.;
PROC. NATL. ACAD. SCI. U.S.A. 92:6077-6081(1995).
-!- SIMILARITY: BELONGS TO THE TFILB FAMILY.
EMBL; U20899; 6836952; -.
TRANSCRIPTION REGULATION; DUPLICATION.
I REPEAT 224 300
SEQUENCE 309 AA; 34756 MW; 0921E52C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLUCOSE INHIBITED DIVISION PROTEIN A.
GIDA OR HI0582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE U
01-MOY-1995 (REL. 32, LAST ANNOTATION
GLUCOSE INHIBITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGASAWARA N., YOSHIKAWA H.;
MOL. MICROBIOL. 6:629-634(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%;
imilarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                        7 Match 90.6%;
Local Similarity 83.3%;
Local Similarity 83.3%;
Local Similarity 83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-168 / CRK2000;
MEDLINE; 92204018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A. MEDLINE; 95320218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIDA.
BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
MEDLINE; 96051385.
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| YRLLIR 6
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| YRLLIR 6
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GIDA_HAEIN
P44763;
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P25812;
                                                                                                                                                                                                                                                                              Query Match
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Matches
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SGD; L0001257; NMD2.
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                                                                                                                                                                                                                                                                                                                                          LT 12
PRC3_DROME
P40301;
                                                                                                   SEQUENCE
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                                             PROC. NATL. ACAD. SCI. U.S.A. 91:9794-9798(1994).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAUDIN M.;
SCIENCE 265:2077-2082(1994).
SCIENCE 265:2077-2082(1994).
-! FUNCTION: INVOLVED IN NONSENSE-MEDIATED DECAY OF MRNAS CONTAINING
-! FREMATURE STOP CODONS. IT INTERACTS, VIA ITS G-TERMING, WITH
NAM7/GPF1. COULD BE INVOLVED IN DETERMINING THE EFFICIENCY OF
TRANSLATIONAL TERMINATION OR REINITIATION OR FACTORS INVOLVED IN
THE INITIAL ASSEMBLY OF AN INITIATION - AND TERMINATION - COMPETENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (REL. 31, CREATED)
01-00V-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 33, LAST ANNORATION UPDATE)
NONSENSE-MEDIATED MRNA DECAY PROTEIN 2 (UP-FRAMESHIFT SUPPRESSOR 2).
NMD2 OR UPF? OR IFST OR SUAL OR YHROU?7(C.
SACCHAROWYCES CEREVISIAE (BAKEY'S YEAST).
EUKARYOTA, FUNGI: ASCOMYCOTINA, HEMIASCOMYCETES.
                                                                                                                                         -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-S28BC / AB972;
MEDLINE; 94378003.
MEDLINE; 94378003.
MEDLINE; 94378003.
MARDISTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J., DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J., KUCABA T., HILLIER L., JIER M., JOHNSTON I., LANGSTON Y., LATREILLE P., LOIS E.J., MACH C., MARDIS E., MOUSER L. WHAN M., RIFKIN L., RIES L., ST PETER H., TREVASKIS E., VAUGHAN K., VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                             SUBUNITS: ALPHA, BETA, BETA', AND BETA".
-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
EMBL: D17510; G1262609;
TRANSCRIPTION: DNA DIRECTED RNA POLYMERASE; CHLOROPLAST.
SEQUENCE 1075 AA; 122470 MW; 7643B7A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                      Score 48; DB 8; Length 1075;
Pred. No. 4.88e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
BMBL: U14974; G555939; -.
EMBL: U12137; G606704; -.
EMBL: U2186; G967213; -.
EMBL: U10556; G500836; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEE S.I., UMEN J.G., VARMUS H.E.;
PROC. NATL. ACAD. SCI. U.S.A. 92:6587-6591(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1089 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95189082.
CUI Y., HAGAN K.W., ZHANG S., PELTZ S.W.;
GENES DEV. 9:423-436(1995).
                                                                                                                                                                                                                                                                                                                                      90.6%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HE F., JACOBSON A.;
GENES DEV. 9:437-454(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U10556; G50083
PIR; S46815; S46815.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-PLY136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE, 95327692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 95189083.
                                                                                                                                                                                                                                                                                                                                                                                                                              1044 frllir 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLLIR 6
                               SUGIURA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMD2_YEAST
P38798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTERSOME 25 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 25 KD SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: IS INVOIVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL PROTECTATIC PATHWAY.
-- SUBJUILIC PATHWAY.
-- SUBJUILIS THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL SUBJUILITY. THE PROTEASOME IS COMPOSED RING-SHAPED STRUCTURE.
-- SUBJUILIAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND ALSO IN THE NUCLEUS.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY TIA; ALSO KNOWN AS THE PROTEASOMES A-TYPE FAMILY. BELONGS TO THE C3 SUBFAMILY.
-- EMBL; X70304; G39780; -- PRICE C3 SUBFAMILY.
-- PRIK; S36116; S36116.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 93363644.
SEELIG A., TROXELL M., KLOETZEL P.M.;
BICCHIM. BIOPHYS. ACTA 1174:215-217(1993).
I- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEFTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLIGHTLY BASIC PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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P36151;
01-70N-1994 (REL. 29, CREATED)
01-7UN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-7UN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 39.4 KD PROTEIN IN CCP1-SIS2 INTERGENIC REGION.
ASP/GLU-RICH (HIGHLY ACIDIC)
                                                                                                                Length 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 234;
                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 7; Length 234. Pred. No. 1.29e+01; 2; Mismatches 0; Indels
                          2 2 D -> YQQ (IN REF. 3 AND 4)
1089 AA; 126746 MW; 4B6ADE8F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
POHL T.M., POHL F.M.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROSOPHILA MELANOGASTER (FRUIT FLY).
EURARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                          Score 47; DB 6; L
Pred. No. 7.98e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA, FUNGI; ASCOMYCOTINA, HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25906 MW; A86BD836 CRC32;
                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLYBASE; FBGN0010405; PROS25.
PROSITE; PS00388; PROTEASOME_A.
PROTEASOME; HYDROLASE; PROTEASE.
                                                                                                          88.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Search completed: Thu May 22 08:29:41 1997 Job time: 12 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHINDZAKI K., OHME M., TANAKA M., WAKASUGI T., HAYASHIDA N., MATSUBAYASHI T., ZAITA N., CHUNWONGSE J., OBOKATA J., YAMAGUCHI-SHINOZAKI K., OHTO., TORAZAWA K., MENG B.Y., SUGITA M., DENO H., KAMOGASHIRA T., YAMAGDA K., KUSUDA J., TAKAIWA F., KATO A., TOHDOH N., SHIMADA H., SUGIURA M.)
EMBO J. 5:2049(1986).

-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATES.
-1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA, BETA', AND BETA".
-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
EMBL; 200044; G1182; --
EMBL; X12745; G11781; --
EMBL; X12745; G11781; --
EMBL; X24865; RNNTE.
--
PIR; A24865; RNNTE.
TRANSCRIPTION: DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
SEQUENCE 1070 AA; 120547 MW; 08C4DF19 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST.
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. BRIGHT YELLOW 4;
MEDLINE; 86192857.
OHME M., CHUNWONGSE J., SHINOZAKI K., SUGIURA M.;
FEBS LETT. 200:87-90(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 8; Length 1070;
Pred. No. 1.29e+01;
2; Mismatches 0; Indels
                                                                                                                                    Length 352;
                                                                                                                              Score 46; DB 11; Length 352
Pred. No. 1.29e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (AUG-1986) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (REL. 06, CREATED)
01-JAN-1998 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
EMBL; 228295; G486541; -.
PIR; S38147; S38147.
PLOTHELICAL PROTEIN.
SEQUENCE 352 AA; 39406 MW; F5B1BB2A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1070 AA.
                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1070 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NICOTIANA TABACUM (COMMON TOBACCO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPOB_SPIOL STANDARD;
P11703;
01-OCT-1989 (REL. 12, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. BRIGHT YELLOW 4;
SUGIURA M.;
                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.8%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1039 frllvr 1044
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1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                              LT 14
RPOB_TOBAC
P06271;
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SEQUENCE FROM N.A.
MEDLINE; 88316931.
HUDGNU T.A., WHITFELD P.R., BOTTOMLEY W.;
J. MOL. BIOL. 200:639-654(1988).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                          OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA(N).

SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA, BETA', AND BETA'.

SIMILARITY BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

EMBL, MS5297; G295121;

PIR; C29959; C29959.

TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.

SEQUENCE 1070 AA: 120899 MW; CDC6F442 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                           CHLOROPLAST.
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CARYOPHYLLALES; CHENOPODIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 8; Length 1070;
Pred. No. 1.29e+01;
2; Mismatches 0; Indels
01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
                                                                                                                   SPINACIA OLERACEA (SPINACH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1039 frllvr 1044
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:42:58 1997; MasPar time 2.50 Seconds 68.327 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-5 (1-6) from US08653294.pep 53 1 RILLRY 6

Description: Perfect Score:

Sequence:

Scoring table:

89912 seqs, 28507787 residues PAM 150 Gap 15 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60

Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir50

Mean 22.859; Variance 32.635; scale 0.700 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Result Query
No. Score Match Length DB ID

Pred. No.

No matches found.

Search completed: Thu May 22 08:43:09 1997 Job time: 11 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:43:26 1997; MasPar time 1.79 Seconds 71.236 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-5 (1-6) from US08653294.pep 53 1 RILLRY 6

Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 23.812; Variance 26.364; scale 0.903 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description В esult Query No. Score Match Length DB Result

Pred. No.

No matches found.

Search completed: Thu May 22 08:43:33 1997 Job time: 7 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:29:58 1997; MasPar time 2.69 Seconds 63.585 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-6 (1-6) from US08653294.pep 53 1 YRLLIR 6 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Mean 22.841; Variance 31.665; scale 0.721 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	5.56e+00	1.30e+01	1.30e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	2.97e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	6.63e + 01	6.63e + 01	6.63e+01	6.63e + 01	6.63e + 01	9.80e+01
Description	DNA helicase YGL150c	hypothetical protein	cell division contro	hypothetical protein	hypothetical protein	hypothetical protein	macrolide 3-0-acyltr	gidA protein - Bacil	glucose inhibited di	MMD2 protein - yeast	multicatalytic endop	hypothetical protein	DNA-directed RNA pol	DNA-directed RNA pol	DNA-directed RNA pol	finger protein rfp -	transforming protein	transforming protein	gene Pl protein - fr	transcriptional acti	hypothetical protein
Ωī	S60416	S50445	A48723	S27599	S56263	S57158	JC4001	BWBSGA	I64078	S48244	S36116	S38147	C29959	RNNTB	548842	S37583	TVHURE	TVHURE	S11034	A42091	S40544
DB	11	77	1	σ	디	디	10	4	ω	11	ഹ	디	ഗ	Н	Ŋ	9	7	72	12	12	ω
Length	1489	101	720	173	221	239	389	628	629	1089	234	352	1070	1070	1078	206	513	801	1030	1638	96
% Ouery Match	96.2	92.5	92.5	90.6	90.6	90.6	90.6	90.6	90.6	88.7	86.8	86.8	86.8	86.8	86.8	84.9	84.9	84.9	84.9	84.9	83.0
Score	51	49	49	48	48	48	48	48	48	47	46	46	46	46	46	45	45	45	45	45	44
Result No.	н	7	m	4	ഗ	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21

##status nucleic acid sequence not shown
##molecule\_type DNA
##residues 757;808-862;865-969;1001-1021;1296-1347;1360-1468
##cross-references EMBL:248618
##

#authors #submission

REFERENCE

22 44 8 23 44 8 24 24 25 24 44 8 25 24 44 8 29 28 24 44 8 33 33 24 44 8 33 34 44 8 33 34 44 8 33 34 44 8 33 34 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 44 43 8 8 44 43 8 8 44 43 8 8 44 43 8 8 44 43 8 8 8 8
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GENETICS

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Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.; Soeda, E.; Yokoyama, K.; Yamazati, M.; Tashiro, H.; Eki, T. submitted to the EMBL Data Library, May 1995
Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 3 - Nostoc sp.
#formal_name Nostoc sp.
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
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02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change
19-Oct-1995
                                                                                                                          #domain MCM2 core domain similarity #label MCM #length 720 #molecular-weight 80184 #checksum 1029
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Y #cross-references EMBL:M81381
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hypothetical protein YFR008w - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walton, D.K.; Gendel, S.M.; Atherly, A.G.
submitted to the EMBL Data Library, February 1992
827599
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##molecule_type DNA
##residues 1-720 ##label MIY
                                                                                 cell division control
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Matches 5; Conservative
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Mol. Biol. Cell (1993) 4:1003-1015
Fission yeast genes ndal(+) and nda4(+), mutations of which lead to S-phase block, chromatin alteration and Ca(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; not compared with conceptual translation
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submitted to the EMBL Data Library, December 1994
Saccharomyees cerevisiae chromosome V cosmids 9871, 8199,
9867, 9495 and lambda clones 6693 and 5898.
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28-May-1993 #sequence_revision 24-Feb-1995 #text_change
24-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A48723 *type complete
cell division control protein nda4 - fission yeast
(Schizosaccharomyces pombe)
#formal.name Schizosaccharomyces pombe
27.Jun-1994 *sequence_revision 27-Jun-1994 *text_change
                                                                                                                                                                                                                                                                                            #map_position 7L
SUMMARY #1ength 1489 #molecular-weight 171454 #checksum 2554
                                                                                                               Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E. submitted to the Protein Sequence Database, May 1996 S64164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #map_position 5L
SUMMARY #length 101 #molecular-weight 12209 #checksum 4508
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hypothetical protein YEL014c - yeast (Saccharomyces
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Pred. No. 1.30e+01;
1; Mismatches 0; Indels
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Pred. No. 5.56e+00;
1; Mismatches 0;
               ##molecule_type DNA
##residues 1-1489 ##label JAA
##cross-references EMBL:272672
                                                                                 ##experimental_source strain S288C
NCE S64153
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##experimental_source strain S288C
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##cross-references EMBL:U18530
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.E.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
#authors Ogasawara, N.; Yoshikawa, H.
#journal Mol. Microbiol. (1992) 6:629-634
#title Genes and thear organization in the replication origin region
of the bacterial chromosome.
#cross-references WUID:92204018
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##cross-references GB:L42023; TIGR:HI0582
##note named as homolog to a protein from Escherichia coli
FFICATION #superfamily gidA protein
XY #length 629 #molecular-weight 70103 #checksum 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164078 #type complete
glucose inhibited division protein (gidA) homolog -
Haemophilus influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
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NMD2 protein - yeast (Saccharomyces cerevisiae)
IFS1 protein; protein FWR0770
#formal_name Saccharomyces cerevisiae
28-oct-1994 #sequence_revision 10-Feb-1995 #text_change
06-Sep-1996
S48244; S46815; S64648; S64738
S48244
He, F.; Jacobson, A.
                                                                                                                                                                                                                            ##INDECTATE OF THE PROBLEM NESS ##CIOSS TEFER OF THE PROBLEM OF TH
                                                                                                                                                    ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 4; Length 0.00, Pred. No. 1.97e+01;
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Nucleotide sequence analysis of the carbomycin biosynthetic genes including the 3-0-acyltransferase gene from
                                                                                                                                                                                                                                                                                                                                                                                                           Rose, M.; Koetter, P.; Entian, K.D. submitted to the Protein Sequence Database, September 1995 857158
                                                                                                                                                                                                                               hypothetical protein J2122
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
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#formal_name Bacillus subtilis
31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
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Pred. No. 1.97e+01;
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hypothetical protein YJR135c
cerevisiae)
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submitted to the EMBL Data Library, September 1994
Identification of a novel component of the nonsense-mediated
mRNA decay pathway using an interacting protein screen.
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Seelig, A.; Multhaup, G.; Pesold-Hurt, B.; Beyreuther, K.;
Kloetzel, P.M.
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multicatalytic endopeptidase complex (EC 3.4.99.46) chain
PROS-Dan5. - fruit fly (Drosophila melanogaster)
proteasome chain PROS-Dan5
#formal_name Drosophila melanogaster
19 - Dec 1993 #sequence_revision 31-Dec 1993 #text_change
19 - May-1995
$36116; $36117; A49550
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factors involved in
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Blochim. Blochys. Acta (1993) 1174:215-217
Sequence and genomic organization of the Drosophila
proteasome PROS-Dm25 gene.
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Pred. No. 2.97e+01;
1; Mismatches 0; Indels
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Favello, T.
submitted to the EMBL Data Library, June 1994
as sequence of S. cerevisiae cosmid 9205.
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Varmus, H.E.
submitted to the EMBL Data Library, May 1995
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A genetic screen identifies cellular retroviral -1 frameshifting.
                                                                                                                                                                                                                                                                                                                           nucleic acid sequence not shown
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##molecule_type DNA
##molecule_type TNA

/ MYQQ',3-1089 ##label VAR
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##residues /MYQQ',3-1089 ##label FAV
##cross-references EMBL:U10556
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##residues 1-234 ##label SE1
##cross-references EMBL:X70304
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Best Local Similarity 83.3%;
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J. Biol. Chem. (1993) 268:25561-25567
Drosophila proteasome Dm25 subunit substitutes the mouse M subunit in hybrid proteasomes. The N-terminal domain is essential for subunit incorporation.

A49550
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#superfamily multicatalytic endopeptidase complex chain
hydrolase; proteinae
#length 234 #molecular-weight 25906 #checksum 7606
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15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
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submitted to the Protein Sequence Database, March 1994
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2; Mismatches 0; Indels
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Pred. No. 4.45e+01;
2; Mismatches 0; Indels
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##experimental_source strain S288C
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Best Local Similarity 66.7%;
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##residues 1-3
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1047 frllvr 1052
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1 YRLLIR
                                                                                                                            #gene
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Shinozaki, K.; Obme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Zaita, N.; Chunwongse, J.; Obckata, J.; Yamaguchi-Shinozaki, K.; Ohto, C.; Torazawa, K.; Meng, B.Y.; Sugita, M.; Deno, H.; Kanogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, N.; Shimada, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal FEBS Lett. (1986) 200:87-90
#title A tobacco chloroplast DNA sequence possibly coding for a polypeptide similar to E. coli RNA polymerase beta-subunit.
#cross-references WIDD:86192857
                                                                                                                                                                                                                                                                                                                    RNNTB #type complete
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - common
tobacco chloroplast
#formal_name chloroplast Nicotiana tabacum #common_name
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohme, M.; Tanaka, M.; Chunwongse, J.; Shinozaki, K.; Sugiura
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The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression. annotation; gene organization, sites, features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S48842 #type complete
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain ; white
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                                                                                                                                                                                                                                                                                                                                                                                                                   30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 03-Feb-1994
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rpoB
chloroplast
#superfamily DNA-directed RNA polymerase beta chain
chloroplast; nucleotidyltransferase
#length 1070 #molecular-weight 120899 #checksum 2671
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                                                                                                                 Score 46; DB 5; Length 1070;
Pred. No. 4.45e+01;
2; Mismatches 0; Indels
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Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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A24865
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1 YRLLIR 6
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| YRLLIR 6
                #genome
CLASSIFICATION
KEYWORDS
SUMMARY
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SUMMARY
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
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Gaps
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chloroplast
#superfamily DNA-directed RNA polymerase beta chain
chloroplast; nuclectidyltransferase; transcription
#length 1078 #molecular-weight 121669 #checksum 2477
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submitted to the EMBL Data Library, October 1994
848842
                                                                                                                                                                                                                                         Length 1078;
                                                                                                                                                                                                                                         Score 46; DB 5; Length 1078 Pred. No. 4.45e+01; 2; Mismatches 0; Indels
                                                          ##residues 1-1078 ##label JUL
##cross-references EMBL:X82417
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                     ##molecule_type DNA
                                                              ##residues
                                                                                                                                                          CLASSIFICATION
KEYWORDS
SUMMARY
  #submission
                    #accession
                                                                                                                                           #genome
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Search completed: Thu May 22 08:30:18 1997 Job time: 20 secs.

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RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAINS-R32.

RA MUCHOPADHYAY P., WILLIAMS J., MILLS D.;

RA MUCHOPADHYAY P., WILLIAMS J., MILLS D.;

RL J. BACTERIOL. 170:5479-5488(1988).

CC -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF HRPM OR OTHER HRP LOCI.

CC -!- SIMILARITY: TO THE C-TERRINAL HALF OF E.COLI MDOG.

DR EMBL; M23555; -; NOT_ANNOTATED_CDS.

DR PIR, A31383; A31383.

KW HYPOTHETICAL PROTEIN.

SEQUENCE 375 AA; 41515 MW; 5FB9D42C CRC32;

CONTRACT OF THE COLUMN                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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SEQUENCE FROM N.A.

STRAIN-BRISTOL N2;

STRAIN-BRISTOL N2;

SUBMATTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.

E-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.

WORMPEP: F54C9:5; CEO255.

RIBOSOMAL PROTEIN; RRNA-BINDING.

SEQUENCE 293 AA; 33386 MW; 8FFEC7EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D20400;
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HYPOTHETICAL 40 KD PROTEIN IN HRP LOCUS (ORFI).
PROKARYOTA, GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.7%; Score 42; DB 8; Length 293; Best Local Similarity 66.7%; Pred. No. 2.15e+01; Matches 4; Conservative 1; Mismatches 1; Indels
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ID YHR4_PSESY
AC P20400;
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Search completed: Thu May 22 08:31:19 1997 Job time: 11 secs.

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1 YRLAIR 6
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| YRLAIR
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YIAJ_HAEIN
P44996;
     TRANSMEM
TRANSMEM
BINDING
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BINDING
SEQUENCE
                                                                                                                                                                    Query Match
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MEDLINE; 90355847.

KOERTNER C., LAUTERBACH F., TRIPIER D., UNDEN G., KROEGER A.;

MOL. MICROBIOL. 4:855-860(1990).

-!- FUNCTION: DI-HEME CYTOCHROME OF THE FUMARATE REDUCTASE COMPLEX.

-!- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING THREE SUBUNITS:

A FLAVOPROTEIN, AN IRON-SULFUR PROTEIN AND A CYTOCHROME B.

-!- SIMILARITY: TO CYTOCHROME B-558 FROM B.SUBTILIS SUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRICARBOXYLIC ACID CYCLE; TRANSMEMBRANE; ELECTRON TRANSPORT; HEME. TRANSMEM 32 54 POTENTIAL.
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Score 42; DB 1; Length 148;
Pred. No. 2.15e+01;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2; Length 223;
Pred. No. 2.15e+01;
2; Mismatches 0; Indels
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;
BACTEROIDACEAE.
                                                                                                                                                                                                                                                                                            CITRUS TRISTEZA VIRUS (ISOLATE T36) (CTV).
VIRIDAE: SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91237334.
SEKIYA M.E., LAWRENCE S.D., MCCAFFERY M., CLINE K.;
GEN. VIROL. 72:1013-1020(1991).
[2]
                                                                                                                                                                                                                     01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-TUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
FUMARATE REDUCTASE CYTOCHROME B SUBUNIT.
                                                                                                                                                                                       223 AA
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larity 66.7%;
Conservative
 85.7%;
Similarity 66.7%;
4; Conservative
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   Query Match
Best Local Similarity
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1 YRLAIR 6
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| YRLAIR 6
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FRDC_WOLSU
P17413;
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Q00686;
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Best Local S
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 95350630.

MEDLINE, 95350630.

MEDLINE, 95350630.

RELESCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., RELESCHMANN R.D., BULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FILL E.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., VENTER J.C., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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CAENORHABDITIS ELEGANS.
EUKRAYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
[1]
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-!- SIMILARITY: STRONG, TO E.COLI YIAJ.
-!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL.
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 268;
                                                                                                                                                                                                  Score 42; DB 4; Length 256; Pred. No. 2.15e+01;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: L45670; G1006264; -.
EMBL: U32784; G926093; -.
PROSITE; PS01051; HTH_LCLR_FAMILY.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-B:
DNA_BIND 37 56 H-T-H MOTIF (POTENTIAL).
SEQUENCE 268 Aa; 30580 MW; B5AA0AEB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 11; 1
Pred. No. 2.15e+01;
2; Mismatches 0;
                                                                HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
101-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1032.
                                                                                                                                                      C3AB8928 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 14
RL5_CAEEL STANDARD; PRT; 293 AA. 1949405.
10.1-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROBABLE 60S RIBOSOMAL PROTEIN L5.
                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         268 AA
  POTENTIAL
                       POTENTIAL.
                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                           M.
                                                                                                                                                                                                  85.7%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                        29723
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
1149
232
232
444
1143
                                                                44
93
143
182
256 AA;
                                                                                                                                                                                                                         Best Local Similarity
Matches 4; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                          188 yrlavk 193
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1141 yrlafr 1146
                                                                                                                                                                                                                                                                                                                                                                         BACTERIOPHAGE T3
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   825
871
1180
1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yrlsik 25
                                                                                                                                                                                     ||||:|
| YRLAIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLAIR 6
                                                                                                                                                                                                                                           RESULT 9
1D V187_BPT3
AC P10302.
DT 01-WAR-1989
DT 01-WAR-1989
DE GENE 18.7.
GS BACTERIOPHA
OC VIRIDAE; DE
RN [1]
RP SEQUENCE FF
RX MEDLINE; 86
RA YAMADA M.,
RL VIROLGY 1!
RN [2]
RN [2]
RN [2]
RN KAMADA M.,
RL VIROLGY 1!
RA YAMADA M.,
RL VIROLGY 1!
SO SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3DHQ_BACSU
P54517;
 ACT_SITE
NP_BIND
ACT_SITE
ACT_SITE
                                                                           SEQUENCE
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                          Best Loc
Matches
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         ARTHUR F.E., VINING L.C.;
J. GEN. MICROBIOL. 139:1785-1793(1993).
J. GEN. MICROBIOL. 139:1785-1793(1993).
I. SEN. MICROBIOL. 139:1785-1793(1993).
I. FUNCTION: CATALYZES THE BIOSYNTHESIS OF 4-AMINO-4-DEOXYCHORISMATE (ADC) FROM CHORISMATE AND GLUTAMINE.
I. PATHWAY: FOLATE BIOSYNTHESIS OF PAMINOBROATE (FABA).
I. SUBUNIT: CONSISTS OF TWO NONIDENTICAL CHAINS: COMPONENT I CATALYZES THE FORMATION OF ADC BY BINDING CHORISMATE AND AMMONIA, COMPONENT II PROVIDES THE GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
EMBL. M64860; G149462; --
LYASE: FOLATE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3-DEHYDROQUINATE SYNTHASE (EC 4.2.1.10)
13-DEHYDROQUINASE), SHIKIMATE 5-DEHYDRATE (EC 4.2.1.10)
(3-DEHYDROQUINASE), SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25), SHIKIMATE KINASE (EC 2.7.1.71), AND EPSP SYNTHASE (EC 2.5.1.19)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARLES I.G., KEYTE J.W., BRAMMAR W.J., HAWKINS A.R.;

NUCLEIC ACIDS RES. 13:8119-8128(1985).

-! FUNCTION: THE AROM POLYPEPTIDE CATALYSES 5 CONSECUTIVE ENZYMATIC

-! FUNCTION: THE AROM POLYPEPTIDE CATALYSES 5 CONSECUTIVE ENZYMATIC

-! REACTIONS IN PRECHORISMATE POLYAROMATIC AMINO ACID BIOSYNTHESIS.

-! PATHWAY: SECOND TO SIXTH SITE IN THE BIOSYNTHESIS FROM CHORISMATE OF THE AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).

-! CATALYTIC ACTIVITY: 7-PHOSPHOAPHOSPHOAD-BEOXY-ARABINO-HEPTULOSONATE = 3-DEHYDROQUINATE + ORTHOPHOSPHOATE.

-! CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.

-! CATALYTIC ACTIVITY: SHIKIMATE + NADP(+) = 5-DEHYDROSHIKIMATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADPH.

-!- CATALYTIC ACTIVITY: ADP + SHIKIMATE = ADP + SHIKIMATE 3-PHOSPHATE.
-!- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE = ORTHOFNEOSPHOSPHATE.

EMBL: X05204: G2333;
-PIR; A24962; BVASA1.

PIR; A24042; A24042.
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X05204; G2332,

REMIN, X05204; G2332,

PIR; A24062; BVASA1.

PIR; A24062; BVASA1.

PROSITE; PS00104; EPSP_SYNTHASE_1.

DR PROSITE; PS01028; DEHYDROQUINASE_1.

DR PROSITE; PS0128; SHIKIMATE_KINASE.

NAROMATIC AMINO ACID BIOSYNTHESIS, MULTIFUNCTIONAL ENZYME;

KW AROMATIC AMINO ACID BIOSYNTHESIS, MULTIFUNCTIONAL ENZYME;

KW AROMATIC AMINO ACID BIOSYNTHESIS, MULTIFUNCTIONAL ENZYME;

NOXIOOREDUCTASE; LYASS; TRANSFERASE; KINASE; NADP; ATP-BINDING.

397 843 EPSP SYNTHASE.

1 384 BPS SYNTHASE.

1 377 3-DEHYDROQUINASE.

1 277 3-DEHYDROQUINASE.

SHIKIMATE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=R153;
MEDLINE; 86176723.
CHARLES I.G., KEYTE J.W., BRAMMAR W.J., SMITH M., HAWKINS A.R.;
NUCLEIC ACIDS RES. 14:2201-2213(1986).
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA: FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
                                                                                                                                                                                                               Score 43; DB 7; Length 470;
Pred. No. 1.28e+01;
                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                  470 AA; 50970 MW; 41AC304B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                     1603 AA.
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 844-1474 FROM N.A.
                                                                                                                                                                                                             87.8%;
llarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                          Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 94014976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86067221
                                                                                                                                                                                                                                                                          411 yriair 416
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| YRLAIR 6
                                                                                                                                                                                                                                                                                                                                                     T 8
ARO1_EMENI
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AROMA OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       Gaps
POTENTIAL.
ATP (BY SIMILARITY).
BY SIMILARITY.
FOMEN A SCHIFF-BASE INTERMEDIATE
(BY SIMILARITY).
W; 26E56D97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE CATABOLIC 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)
                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                  Score 43; DB 1; Length 1603;
Pred. No. 1.28e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 10; Length 83;
Pred. No. 2.15e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XAMADA M., FUJISAWA H., KATO H., HAMADA K., MINAGAWA T., VIROLOGY 154:246-246(1986).
EMBL: M14784: G1196765; -
PIR: E23476; WBBPT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAMADA M., FUJISAWA H., KATO H., HAMADA K., MINAGAWA VIROLOGY 151:350-361(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                               VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PODOVIRIDAE
                                                                                                                                                                                                                                                                                                                                          (REL. 10, LAST SEQUENCE UPDATE)
(REL. 10, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6D9B1F91 CRC32;
                                                                                                                                                                                                                                                                                           83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                           CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 AA; 9393 MW;
                                                                                  1603 AA; 175094
                                                                                                                  / Match 87.8%;
Local Similarity 83.3%;
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 85.7%;
Local Similarity 66.7%;
les 4; Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
   825
878
1180
1208
                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (REL. 10,
01-MAR-1989 (REL. 10,
01-MAR-1989 (REL. 10,
GENE 18.7 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86209997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS SUBTILIS
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297 AA

PRT;

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STANDARD;
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1 YRLAIR
RL1_YEAST
P26321;
                                                                                                                                                                               SEQUENCE MEDLINE;
                                                                                                                                                                                                     TANG B., J. BIOL.
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 g
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                                                                                                                                                                              GENE 122:381-382(1992).
-!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                              ACTIN AND TUBULIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBURIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
-!- SIMILARITY: TO OTHER MEMBERS OF TCP-1 CHAPERONIN FAMILY.
EMBL; D11351; G217871; -.
PROSITE; PS00750; TCP1_1.
PROSITE; PS00751; TCP1_2.
PROSITE; PS00955; TCP1_3.
CHAPERONE; ATP-BINDING; MULTIGENE FAMILY.
SEQUENCE 545 AA; 59229 MW; 8E52A94B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MICHAEL W.A., DREYEVES G.;
J. BIOL. CHEM. 271:11571-11574(1996).
-i - FUNCTION: THIS PROTEIN BINDS SS RNA.
-i - STHILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
EMBL: U48270; G1206017; -.
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                     01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA).
                                                                                          ARĀJIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA: PLANTA: EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                    ŠEČUENCE FROM N.A.
MEDLINE; 93138412.
MORI M., MURATA K., KUBOTA H., YAMAMOTO A., MAISUSHIRO A.,
MORITA T.;
                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 9; Length 545;
Pred. No. 7.58e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 8; Length 293; Pred. No. 1.28e+01; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AA; 33255 MW; 4D72400A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
60S RIBOSOMAL PROTEIN LS.
                     545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                     PRT;
                                                                                                                                                                                                                                                                                                                                                        Query Match 89.8%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.8%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOMAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                124 yrlamr 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 yrlvvr 53
                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLAIR
    RESULT 4
TO TCPA_ARATH
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RESULT

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STORMER R. K., VO D.H., WANG Y., WINNETT E.;
STORMER R. K., VO D.H., WANG Y., WINNETT E.;
SUBMITTED (DEC-1995) FOR EML/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: THIS PROTEIN BINDS 58 RNA.
-!- FUNCTION: THIS PROTEIN BINDS 58 RNA.
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
REMBL; M65065; G173235; --
REMBL; M65065; G173235; --
REMBL; M05066; G172424; --
REMBL; M04864; G173235; --
REMBL; M04964; G173235; --
REMBL; M04969; G172424; --
REMBL; M04909; RPL1.
R PIR; S14172; S40899; RPL1.
R SGD; L0001699; RPL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                  60S RIBOSOMAL PROTEIN L1 (L5) (YL3) (RIBOSOMAL 5 S RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 93233645.
DESHWUKH M.P., TSAY Y.F., PAULOVICH A.G., WOOLFORD J.L.;
MOL. CELL. BIOL. 13:2835-2845(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 112 R -> K (IN REF. 4 AND 5).
297 AA; 33743 MW; 2D9F1304 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TZACOLOFF A., CAPITANIO N., NOBREGA M.P., GATTI D., EMBO J. 9:2759-2764(1990).
                                                                                       PROTEIN).

RPL1 OR YPL131W OR LPI14W.
SACCHAROWYCES CEREVISTAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.8%; Score 43; DB 8; LA Best Local Similarity 66.7%; Pred. No. 1.28e+01; Matches 1; Mismatches 1.
                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                    FROM N.A.
92388126.
NAZAR R.N.;
CHEM. 267:17738-17742(1992)
                                                                                                                                                                                                                     STRAIN-S288C;
MEDLINE; 91177855.
TANG B., NAZAR R.N.;
J. BIOL. CHEM. 266:6120-6123(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOSOMAL PROTEIN; RRNA-BINDING.
    CREATED)
01-MAY-1992 (REL. 22,
01-MAY-1992 (REL. 22,
01-OCT-1996 (REL. 34,
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 90360986.
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              LDL-RECEPTOR CLASS A 5 (PARTIAL).
LDL-RECEPTOR CLASS A 6 (PARTIAL).
LDL-RECEPTOR CLASS A 7.
C.TERMINAL SERINE PROTEASE-LIKE.
LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 11.
LDL-RECEPTOR CLASS A 11.
CELL ATTACHMENT SITE (POTBNIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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GLYCOSAMINOGLYCAN (POTENTIAL).
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Pred. No. 4.44e+00;
0; Mismatches 1; Indels
  SERINE/THREONINE-RICH DOMAIN
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                                                                                           MEDLINE; 83189071.

SEQUENCE FROM N.A.

MEDLINE; 83189071.

SANGER F., COULSON A.R., HONG G.F., HILL D.F., PETERSEN G.B.;

J. MOL. BIOL. 162:729-773(1982).

-!- FUNCTION: GENE J PROTEIN MAKES UP THE DISTAL FIBER OF THE PHAGE
TAIL. IT IS RESPONSIBLE FOR ADSORPTION TO THE HOST DUBING
INFECTION AND DEPERMINES HOST SPECIFICITY. IT SPECIFICALLY BINDS
TO THE LAMBDA RECEPTOR PROTEIN OF E.COLI K12.

-!- UNDER THE ACTION OF THE GENE G, T, H, M, L, K, AND I PROTEINS,
C. GENE J PROTEIN SERVES AS THE INITIATOR OF TAIL POLYMERIZATION.
THERE ARE 2-4 COPIES OF PROTEIN J PER MATURE PHAGE.

REMBL; JOA459, GSBPL.

RP PIR; A04374; QSBPL.

SEQUENCE 1132 AA; 124422 MW; E44CCD6E CRC32;
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CELL 82:785-794(1995)
-!- FUNCTION: UDDEL, PIDE AND WINDBEUTEL TOGETHER TRICGER THE PROTEASE
-!- FUNCTION: UDDEL,
CASCADE WITHIN THE EXTRAEMBRYONIC PERIVITELLINE COMPARTMENT WHICH
INDUCES DORSOVENTRAL POLDARITY OF THE DROSOPHILA EMBRYO. NUDEL IS
DIRECTLY INVOLVED IN LOCALLY PRODUCING THE TOLL LIGAND.
-!- TISSUE SPECIFICITY: FOLLICLE.
-!- PTM: REQUIRES CLEAVAGE FOR ACTIVATION (PRESUMABLY).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-!- SUBLEMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
-!- SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
EMBL; U29153; G984321; --
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WIID 2.
WIID 3.
WIID 5.
WIID 6.
WIID 6.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 3.
CATALYTIC.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
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FLYBASE; FBAN0002926; NDL.
SERINE PROTEASE; GLYCOPROTEIN; SIGNAL; DEVELOPMENTAL PROTEIN;
HYDROLASE; REPEAT; ZYMOGEN; EXTRACELLULAR MATRIX.
SIGNAL

44 2616 SERINE PROTEASE NUDEL.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 10; Length 1132;
Pred. No. 4.44e+00;
2; Mismatches 0; Indels
                                      BACTERIOPHAGE LAMBDA.
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; SIPHOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SERINE PROTEASE NUDEL PRECURSOR (EC 3.4.21.-)
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STRAIN-OREGON-R; TISSUE-OVARY;
MEDLINE; 95401268.
                                                                                                                                                                                                                                                                                                                                                                                                                         91.8%; (larity 66.7%; ) Conservative
HOST SPECIFICITY PROTEIN
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Matches 4; Conserv
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| YRLAIR 6
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P98159;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:31:08 1997; MasPar time 1.96 Seconds 64.775 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-7 (1-6) from USO8653294.pep 49 1 YRLAIR 6 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

59021 segs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 22.440; Variance 22.471; scale 0.999 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	2.57e+00	4.446+00	7.58e+00	1.28e + 01	1.28e+01	1.28e+01	1.28e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01
Description	RETRO	SERINE PROTEASE NIDEL	T-COMPLEX PROTEIN 1,	60S RIBOSOMAL PROTEIN	60S RIBOSOMAL PROTEIN	PARA-AMINOBENZOATE SY	PENTAFUNCTIONAL AROM	GENE 18.7 PROTEIN.	PUTATIVE CATABOLIC 3-	COAT PROTEIN.	FUMARATE REDUCTASE CY	HYPOTHETICAL TRANSCRI	PROBABLE 60S RIBOSOMA	HYPOTHETICAL 40 KD PR	DNA POLYMERASE III, B	DNA POLYMERASE III, B	C4-DICARBOXYLATE TRAN	ALPHA-ADAPTIN (C) (CL	ALPHA-ADAPTIN (C) (CL	LOCOMOTION-RELATED PR	ALPHA-ADAPTIN (A) (CL
ei ei	RDPO_SCHPO	NDI DROME	TCPA_ARATH	RL5_SCHPO	RL1_YEAST	PABB_LACLA	ARO1_EMENI	V187_BPT3	3DHQ_BACSU	COAT_CTV36	FRDC_WOLSU	YIAJ_HAEIN	RL5_CAEEL	YHR4_PSESY	DP3B_MYCSM	DP3B_MYCLE	DCTB_RHIME	ADAC_RAT	ADAC_MOUSE	HIG_DROME	ADAA_MOUSE
DB	١٠٥	2 6	σ	ω	∞.	7	Н	10	н	N	4	11	ω	11	m	m	ო	Н	Н	ß	П
% Query Match Length	1333	2616	545	293	297	470	1603	83	148	223	256	268	293	375	397	399	621	937	938	928	977
% Query Match	93.9	91.0	89.8	٠	7	87.8	7	85.7	85.7	85.7	85.7		85.7		85.7				85.7	85.7	
Score	46	4. 4. U 10.	44	43	43	43	43	42	42	42	42	42	43	42	42	42	42	42	42	42	42
Result No.	rd (	7 m	4	'n	φ	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22

2.15e+01 2.15e+01 2.15e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01 3.56e+01	. 56e
PAIRED AMPHIPATHIC HE ADENTLATE CYCLASE (EC HIGH-MOLECULAR-WEIGHT NITROGEN REGULATION P HOTOSYSTEM Q(B) PROT PHOTOSYSTEM Q(B) PROT P	TEIN-TYROSINE PH
SIN3 YEAST CYAA_SCHPO NTRB_SCHPO NTRB_SCHLY NTRB_SCHLY NTRB_SCHLY PSBA_MRRPO PSBA_RTRDI PSBA_RTRDI PSBA_RTRDI PSBA_FREDI	
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84844444444444444444444444444444444444	

### ALIGNMENTS

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Gaps
                                                                                                                                                     STRAIN-972;
MEDLINE; 93380663.
WEAVER D.C., SHPAKOVSKI G.V., CAPUTO E., LEVIN H.L., BOEKE J.D.;
GENE 131:135-139(1993).
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STAINS—972;
MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!-SIMILARITY: REGIONALLY, TO PROTEASE, REVERSE TRANSCRIPTASE,
RNASE H AND
RETROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                 1 400 TO CAPSID PROTEIN FROM RETROVIRUSES.
206 206 L -> P (IN REF. 1).
1333 AA; 154932 MW; 78D5D7DA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 8; Length 1333;
Pred. No. 2.57e+00;
1; Mismatches 0; Indels
                    00554;
01-00T-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
SETROTRANSPOSABLE ELEMENT TF2 155 KD PROTEIN.
SPAC208A: 13C.
SCHIZOSACCHAROWCES PONBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1333 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                             EMBL; L10324; G173439; -. EMBL; Z69240; E220685; -. TRANSPOSABLE ELEMENT.
            STANDARD;
                                                                                                                                          SEQUENCE FROM N.A.
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RDPO_SCHPO
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 1.92 Seconds 34.026 Million cell updates/sec Thu May 22 08:30:35 1997; Run on:

not generated Tabular output

>US-08-653-294-6 (1-6) from US08653294.pep 53

Description: Perfect Score:

1 YRLLIR 6 PAM 150 Gap 15 Scoring table: Sequence:

92623 segs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq26 Database:

|:part| 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19

Mean 16.490; Variance 45.535; scale 0.362 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	+01	+01	+01	+01	+01	+01	+01	29e+02	66e+02	+02	+02	66e+02	66e+02	+05	66e+02	66e+02	+02	+02	+02	15e+02
Pred. No	4.52e+01	5.89e+01	5.89e+01	5.89e+0	7.66e+0	7.66e+01	9.94e+01	1.29e	1.66e	1.66e+02	1.66e+02	1.66e	1.66e	1.66e+02	1.66e	1.66e	1.66e+02	1.66e+02	2.15e+02	2.15e
Description	3-acylation enzyme.	Bacillus thuringiensi	Nonsense-mediated mRN	Nonsense-mediated mRN	Drosophila-12 cadher	Protocadherin clone D	Erythrobacter longus	Virulence gene cluste	Peptide fragment (1.0	HPV18 E6/E7 proteins.	HPV-18 E6 protein.	HPV 18 E6 protein fra	Human calcium channel	Human amphotropic ret	Glucosyltransferease	Rianodin receptor.	MH mutant porcine rya	Ryanodine receptor de		HLA-B2702 84-75-84 pa
dī	R15428	R93081	W01897	W01896	R58902	R87142	R95698	R97246	R61548	R63866	R79656	R27728	R27642	R63808	R32925	R10834	R25450	R11510	R95429	R95428
DB	ო	18	19	13	1	17	18	13	11	12	14	'n	'n	12	φ	ო	Ŋ	7	18	18
Match Length DB	389	724	764	1089	43	43	434	4472	10	158	158	271	451	652	1592	4987	5035	5072	12	20
Match	90.6	88.7	88.7	88.7	86.8	86.8	84.9	83.0	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	79.2	79.2
Score	48	47	47	47	46	46	45	44	43	43	43	43	43	43	43	43	43	43	42	42
NO	П	7	m	4	S	ø	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20

2.15e+02	7 -	감	7	7	ς:	۳.	7	7	2.15e+02	.15	2.76e+02	۲.	۲.	2.76e+02	۲.	۲.	2.76e+02	.76	۲.	۲.	2.76e+02	3.54e+02	3.54e+02
82702	115	32702 CIL modula	Hydrophobic protein d	EpiQ protein.	snaC gene product inv	_	67-kD protein toxin.	Enzyme M-11.	Enzyme Q36.	GAP protein Ira2.	Zebrafish sonic hedge	Murine monoclonal ant	ATP-sensitive K chann	E.coli cell division	Nocardia corallina al	Nocardia corallina al	GC-B.	NPRB(Pro655, Glu656,	Human Natriuretic Pep	Sequence of clone HIV	Sequence encoded by t	do stra	tie receptor kinase.
R95430	000000	R92911	22	33	20	73	P91462	4	55	R59926	R78151	R93159	R63233	R78184	R66215	R81471	m	R10867	R10399	P93283	P81769	W05507	R39820
81.	9 4	191	7	7	10	18	-	12	12	11	15		12	14	13	17	œ	ო	ო	Н	Н	13	œ
20	2 6	202	78	202	402	643	643	772	775	3079	64	108	391	457	501	501	1025	1047	1047	3077	3211	169	1138
79.2												77.4	77.4	77.4	77.4		77.4	77.4	77.4			75.5	75.5
24		42					42	42	42		41	41	41	41	41	41	41	41				40	
21	7 6	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Okamura K;

Namura K;

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                                                                                                                     A acylation enzyme.

Macrolide antibiotics; acylation; Streptomyces; tylosin;
Spiramych; leucomycin; nidamycin; acyA.

Streptomyces thermotolerans ATCC 11416.

N EP-45955-A.

O4-DEC-1991; 109033.

R 22-FEB-1991; JP-048753.

A (SAOC ) MERCIAN CORP.

A AISAWA A, KAWAMULA N, KOjima I, Tone H, Okamoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .r. 2
1908: standard; Protein; 724 AA.
R93081;
04-0CT-1996 (first entry)
Bacillus thuringlensis insecticidal protein JEG80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 3; Le
Pred. No. 4.52e+01;
1; Mismatches 0
                                        Ą.
JT 1
R15428 standard, Protein, 389
R15428.
25-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 yrlllr 163
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| YRLLIR 6
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ID R9
AC R9
DT 04
DE B8
RESULT
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NPENDS, 06893.

NPENDS, 06893.

NPENDS, 06893.

POINTUCLEOTIES sequences encoding new proto:cadherins - useful polynucleotide sequences encoding me proto:cadherins - useful polynucleotide sequences encoding and regulating activities.

Example; Page 63; 114pp; English.

Example; Page 63; 114pp; English.

Tor regions of conserved As sequence, one from the middle of the corresp. Corresp. Condomain (EC-3) and the other from the corresp. Corresp. Gegenerate oligos (06894), 068950) were designed for use as PCR primers. PCR was carried out on a rat brain condomain (ED-3) and the other from the condomain (ED-4) were corresp. Two major bands of about 450 bps and 130 bps were found. The 450 bp band corresponded to the expected length between the two primer sites, but the 130 bp band could not be predicted from any of the previously identified cadherin sequences. The 450 bp and 130 bp bands were extracted and sequenced. Nineteen novel partial cDNA clones were isolated. The DNA and deduced As sequences of the corresp. to the PCR primers) are given in 068951-068969 and R58860-R58878. Various cDNA fragments structurally similar to the rat cDNAs were isolated from human, structurally similar to the rat cDNAs were isolated from human, couse and Kenopus brain cDNA prepns. by PCR using the above primers. The DNA and deduced As sequences corresp. to the PCR primers) are given in the DNA and deduced and R5882-R58905 and R49143. Comparison of the deduced As sequences indicates a similarity, in particular,
                                                                                                                                                                                                                                                                                                                                                                                                                            isolated nonsense-mediated mRNA decay gene and protein - used to develop methods for inhibiting the decay pathway for producing heterologous or endogenous proteins.

Claim 8; Page 49-52; 73pp; English.

The NMD2 gene (T31993) is named after its role in the Nonsense-Mediated mRNA becay pathway. The protein, NMG2p, binds to Upfip.

A C-terminal fragment of the protein (T31994) also binds Upfip and, when overexpressed in the host cell, the fragment inhibits the function of Upfip, thereby inhibiting the nonsense-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 19; Length 108
Pred. No. 5.89e+01;
1; Mismatches 0; Indels
                                                                                              Nonsense-mediated mRNA decay 2 protein.
Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1995 (first entry)
Drosophila-12 cadherin-related molecule.
Cadherin; cell adhesion molecule.
                                                                                                                                                                                         WO9622301-A1.
25-JUL-1996.
27-DEC-1995; U16930.
20-JAN-1995; US-375300.
(UYMA-) UNIV MASSAHUSETTS MEDICAL CENT.
He F. Jacobson AS;
WPI; 96-354469/35.
      standard; Protein; 1089 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T
R58902 standard; Protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                     (first entry)
                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1993; U12588.
29-DEC-1992; US-998003.
(DOHE-) DOHENY EYE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA decay pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 yrilir 585
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T31993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-1994.
                                                                  24-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R58902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                          New B.thuringiensis ser. jegathesan insecticidal proteins - and related DNA, with high activity against dipteran larvae, e.g.

T related DNA, with high activity against dipteran larvae, e.g.

T Amegyptit, A.stephensi or C.pipiens
Claim 17: Fig 5: 55pp; French.
C flaim 17: Fig 5: 55pp; French.
C from Bacilius thuringiensis ser. jegathesan 367 (Btjeg367); it is a crystal toxin of mol. wt. 80 kD which is active against dipteran insects, esp. mosquitoes. The full-length, recombinant JEG80 toxin, chad mean LC50 values (in ng/ml) after 48 hours of 18.8, 42.7 and 10.1 against larvae of Aedes aegypti, Anopheles stephensi and Culex pipiens, respectively. Wild-type Btjeg367 crystals gave values of 47.4, 54.5 and 9.6. The JEG80 protein is far more toxic (6-40 times coxin, despite their close sequence similarity.
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27-JUL-1996...
20-JAN-1995; US-375300.
20-JAN-1995; US-375300.
30-JAN-1995; US-375300.
30-JAN-1995; US-375300.
31-JACODSON AS;
31-JACODSON AS;
32-JUL-1994.
33-JUL-1994.
33-JUL-1994.
34-JUL-1994.
35-JUL-1994.
35-JUL-1994.
36-JUL-1994.
36-JUL-1994.
36-JUL-1994.
37-JUL-1994.
38-JUL-1994.
38-JUL-1996...
38-JUL-1
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Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae; Aedes aegypti; Anopheles stephensi; Culex pipiens; Btjeg 367.
Bacillus thuringiensis ser. jegathesan 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 5.89e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.89e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonsense-mediated mRNA decay 2 C-terminal.
Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r 3
W01897 standard; Protein; 764 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.7%;
83.3%;
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Similarity 83.3%;
5; Conservative
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                                                                                                                       29-FEB-1996.
24-AUG-1995; F01116.
25-AUG-1994; FR-010299.
(INSP ) INST PASTEUR.
Delecluse A, Thiery I;
WPI; 96-151374/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae, WO9622301-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 yrliir 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 yrillir 260
                                                                                                                                                                                                                                                                                                       N-PSDB; T17044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLLIR 6
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Matches

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Gaps

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Length 1089;

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T
R95698 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynuciectide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities asample 2; Page 67-68; 146pp; English.

RR142-RR144 represent partial fragments of the drosophila protocadherin sequence. The cDNAs encoding these sequences were isolated after conscienting a drosophila whole body CDNA preparation with the primers shown in T03575 and T03576. The primers were constructed from portions of the amino acid sequences of the third and fourth extracellular domains of published cadherin sequences. The cytoplasmic domain of cadherins of interacts with the cytoplasmic domains and other cytoplasmic domains and cadherins adhesive function. The cadherins which do not possess a cadherins absive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cell-cell adhesion. These sequences may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                             29-AUG-1996 (first entry)
Protocadherin clone DROSOPHILA-12.
Protocadherin, pos3; po4; po5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly.
Drosophila melanogaster.
                                                                                                     ö
there are three sets of clones that appear to be cross-species homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and HUMAN-11; and MOUSE-326 and HUMAN-42.
                                                                                                       Gaps
                                                                                                     ;
0
                                                                       Score 46; DB 11; Length 43;
Pred. No. 7.66e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 17; Length 43;
Pred. No. 7.66e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                    standard; Peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
ilarity 83.3%;
Conservative
                                                                       Query Match 86.8%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by ATG"
Misc_difference 40
Misc_difference 41
/note= "encoded by ACA"
Misc_difference 42
/note= "encoded by GC"
Misc_difference 42
/note= "encoded by GGC"
Misc_difference 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1995; U08071.
27-JUN-1994; US-268161.
                                                                                                                                                                                                                                                                                                                                     Misc_difference 38
/note= "encoded by
Misc_difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96-068873/07.
                                            43 AA;
                                                                                                                                 yrlvir 16
                                                                                                                                                   1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encode WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JAN-1996
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                    LT 6
R87142 s
R87142;
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Erythrobacter sp. phytoene dehydrogenase and lycopene cyclase genes
for the prodn. of beta-carotine useful as a food colourant
for the prodn. of beta-carotine useful as a food colourant
for the prodn. of beta-carotine useful as a food colourant
for the prodn. of beta-carotine useful as a food colourant
for the prodn of the product of the lycopene cyclase enzyme from
Erythrobacter longus ARCC 14126. The corresp. gene was isolated from an
Erythropanase gene from Erwinia hebicola as a probe. The probe isolated
a nucleotide fragment which contained two open reading frames (ORF).
CORF2 (1578 bp) encodes the phytoene dehydrogenase (137198) whereas ORF1
(1302 bp) encodes lycopene cyclase. The two ORFs were inserted into the
plasmid pRR415 to generate pRKCD. This plasmid was transformed into
Rhodobacter sphaeroides for prodn. of the proteins. The phytoene
dehydrogenase and lycopene cyclase can be used to produce beta-carotine
for use as a food colourant or as a food additive with anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
20-SEP-1996 (first entry)
Erythrobacter longus lycopene cyclase protein.
Phytoene dehydrogenase; Erythrobacter longus; Erwinia hebicola; probe; open reading frame; lycopene cyclase; Rhodobacter sphaeroides; beta-carotine; food colourant; additive; anti-cancer.
507803241-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEI; 96-287194/29.
Identifying virulence genes in microorganisms - by introducing mutants with insertion inactivated genes into environment and mutants with insertion inactivated genes into environment and trainstant and analysis of mutants.

A method for identifying a microorganism having a reduced adaptation to a particular environment comprising the steps of: (1) providing a plurality of microorganisms each of which is independently mutated by the insertional inactivation of a gene with a nucleic acid comprising a unique marker sequence so that each mutant contains a different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1997 (first entry)
Virulence gene cluster polypeptide product.
Mutant; adaptation; virulence factor; identification; screening;
Vaccine; drugs; infection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 18; 1
Pred. No. 9.94e+01;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "All x's in this sequence correspond termination codons in the virulence gene cluster sequence given in T09224."
W09617951-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 8
R97246 standard; Protein; 4472 AA.
R97246;
                                                                                                                                                                                                                                                 03-5E-1994, 236621.
30-SEP-1994, JP-236621.
(ASAH ) ASAHI KASEI KOGYO KK.
WPI; 96-233337/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-DEC-1995; G02875.
09-DEC-1994; GB-024921.
31-AN-1995; GB-001881.
05-MAY-1995; GB-009239.
(RPMS-) RPMS TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; drugs; infect
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 yrllar 345
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Gaps

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Best Local Similarity
Matches 5; Conserv

11 yrlvir 16

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T 10
R63866 standard; Protein; 158 AA.
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marker sequence, or clones of the said microorganism; (2) providing individually a stored sample of each mutant produced by step (1) and providing individually stored nucleic acid comprising the unique marker sequence from each individual mutant; (3) introducing a plurality of mutants produced by step (1) into the said particular environment and allowing those microorganisms which are able to do so to grow in the said environment; (4) retrieving microorganisms from the said environment; (4) retrieving microorganisms from cucleic acid from the retrieved microorganisms; (5) comparing any marker sequences in the nucleic acid isolated in step (4) to the unique marker sequence of each individual mutant stored as in step (2); and (6) selecting an individual mutant which does not contain any colthe marker sequences as isolated in step (4). The products and methods can be used for identifying virulence genes in microorganisms. The mutant microorganisms can be used in vaccines or to screen for drugs which reduce virulence or compounds useful for preventing, sequence 4472 AA;
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases.

Example 5: Page 109: 138pp; English.

R59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1

Binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (R71293).

R61548 has an 1050 of 0.0036 and the sequence occurs at position 24 in the HPV E6 protein. The peptides of the invention can induce cytocoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Til-MAY-1995 (first entry)
Peptide fragment (1.0914) of HPV binds HLA-A2.1.
Peptide fragment (1.0914) of HPV binds HLA-A2.1.
antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HHIVI; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen; surface antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; lomer; anchor; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                motif - used
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 19; Length 4472;
Pred. No. 1.29e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic peptide(s) having an HLA-A2.1 binding motif - \iota for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 11; Length 10;
Pred. No. 1.66e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1994.
04-MAR-1994; U02353.
05-WAR-1993; US-027146.
04-JUN-1993; US-073205.
29-NOV-1993; US-159184.
(CYTE.) CYTEL CORP.
GTCY HM, KAST WM, Sette A, Sidney J; WPI; 94-302678/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 9
R61548 standard; peptide; 10 AA.
R61548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.1%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                        Query Match 83.0%;
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer or lymphoma, etc.
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Best Local Similarity
Matches 5; Conserv
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| YRLLIR
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Matches
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Disclosure; Page 100-101; 157pp; English.

HPV-18 E GONA (diven in Q97848) was amplified from a HeLa cell CDNA library using the primers given in Q97846-47. The gene was subcloned into a baculovirus vector for expression of recombinant E6 in Sf9 insect cells for use as a component of an sequence 158 AA;
                                                                                                                                                                                                                                                                                                              detector probe
Disclosure; Page 27-28; 79pp; English.
The sequences of the E6 and E7 polypeptide-encoding regions of human papillomavirus (HPV) 16 and 18 are given in 075470-71 and the encoded proteins in R63865-66, respectively. Probes and primers encoded proteins in R63865-66, respectively. Probes and primers based on these sequences were used for HPV infection diagnosis; expression of E6 and E7 is diagnostic for cervical cancer or pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
R63866;
28-JUN-1995 (first entry)
HPV18 E6/E7 proteins.
HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dyplasia;
                                                                                                                                                                                                                                                                         Human papilloma virus detection assay – by amplification using self sustained sequence replication and hybridisation with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPV-18 E6 protein.
Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;
cell proliferation; cancer; psoriasis; fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rolfe M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 12; Length 158
Pred. No. 1.66e+02;
0; Mismatches 1; Indels
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Pred. No. 1.66e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cottarel G, Draetta G, Eckstein JW,
WPI; 95-255137/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 11
R79656 standard; Protein; 158 AA.
R79656;
                                                                                                Human papillomavirus strain 18
WO9426934-A.
                                                                                                                                                                                         (BAXT ) BAXTER DIAGNOSTICS INC
Brown JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1995 (first entry)
                                                                                                                                                       06-MAY-1994; UO5085.
06-MAY-1993; US-058920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1994; US-305520.
(MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1994; US-247904
27-MAY-1994; US-250795
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                                                                                                                                                                                                                                   WPI; 95-006821/01.
P-PSDB; Q75471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignant states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 ynllir 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JAN-1995;
04-JAN-1994;
                                                                                                                                      24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
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Gaps

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Length 451; Indels

RESULT

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Peptide

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Definition Circuit Wan ZEIJL M, O'hara BM;
NPISOB, 374311.

NPISOB, 074311.

PT Nucleic acid sequence encoding an amphotropic retrovirus receptor
PT used to create viral vectors useful in gene therapy.

Claim 4; Fig 2; 24pp; English.

CQ 4311 encodes R63808 the amphotropic retrovirus receptor gibbon cleukaemia virus receptor 2 (GLNR2). Nucleotide fragments of Q74311

Can be used to create vectors, for use in human gene therapy and can be used to create vectors, for use in human gene therapy and GLNR2 gene and receptor. The nucleotide fragments can also be used as probes to study GLVR2 distribution in cells from various species.
Human neuroblastoma cell line, hippocampus, frontal and temporal cortex and visual cortex cDNA banks were screened with a probe containing carp skeletal muscle Ca-channel cDNA. The cDNA clone p1247-10.1.1.1 was sequenced and found to encode amino acids 1050 1512 including the end of the third domain (IIIs6) and the entire bomain IV and about 130 C-terminal flanking amino acids which correspond to the last cytoplasmic part of the protein. The human neuronal calcium channel proteins can be used for screening for calciumal ligands (agonists or antagonists). See also 029259-029275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human amphotropic retrovirus receptor GLVR2.
Amphotropic retrovirus receptor; gibbon leukemia virus receptor 2; GLVR2; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence glucosyl:transferase-I - comprises Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 12; Length 652;
Pred. No. 1.66e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                           Score 43; DB 5; Leng
Pred. No. 1.66e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucosyltransferease I.
GT-1; Streptococcus; dental; caries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R63808 standard; Protein; 652 AA.
R63808;
28-JUN-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-WAR-1994; 104889.
16-APR-1993; US-050684.
(AMCY ) AMERICAN CYANANID CO.
Johann SV, Ohara BM.
                                                                                                                                                                                                                                                                                                                                           81.1%;
larity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.1%;
|larity 83.3%;
|Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-1991; 186592.
25-JUL-1991; JP-186592.
(FUKU/) FUKUI I.
(KATC/) KATC K.
WPI; 93-079449/10.
N-PSDB; Q37760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus sobrinus
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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28-JUN-1993
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                                                                                                                                                                                                                                                                                     Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant virus vectors encoding human papillomavirus proteins

recombinant virus vectors encoding human papillomavirus proteins

recombinant virus vectors encoding against HPV infections and

recombinant virus caused by them, such as cervical cancer

bisclosure; Fig 1b; 83pp; English.

The fragment of DNA contg, the HPV-18 E6/E7 coding region was

prepd. by PCR from plasmid pBR322/HPV16 (Boshart et al., EMBO J. 3;

[15] using oligonuclectides Sol and Sol. The prod. of the
second reading frame is the HPV-18 E6. The E6 and E7 ORFs are fused

reading frame encodes HPV-18 E6. The E6 and E7 ORFs are fused

reading frame encodes HPV-18 E6. The E6 and E7 ORFs are fused

reading frame of the HPV-18 E6. The E6 and E7 ORFs are fused

codens of the HPV E7 sequence. The single ORF of the TPV-18 E6/E7 may be
inserted into vaccinia virus DNA at neutral sites (pref. by inserting

two sets of the DNA in opposite orientations to overcome the problem

of intertypic recombination) to make a recombinant virus vector for
ganish HPV. See also R27723-43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 5; Lengtn 2,2,
Pred. No. 1.66e+02;
                                                                                                                                                                                                            09-MAR-1993 (first entry)
HPV 18 E6 protein fragment.
Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification; immunotherapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER AG.
Franc J, Rae P, Unterbeck A, Weingaertner B,
WPI; 9233446/41.
P-PSDB, R27642.
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/note= "encoded by GNN codon, N is unknown"
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Human calcium channel 27980/4.

Plasmid p1247-10.1.1.1; Ca-flux assay; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1991; G00424.
14-MAR-1991; GB-005383.
(IMMU ) IMMUNOLOGY LID.
Boursnell MEG, Inglis SC, Munro AJ;
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Claim 2; Page 24-27; 101pp; German
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R27642 standard; Protein; 451 AA.
R27642;
                                                                                                                                                  R27728 standard; Protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 81.1%;
Local Similarity 83.3%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "HPV-18 E6 protein"
WO9216636-A.
                                                                                                                                                                                                                                                                                                                                           Human papillomavirus 18
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07-0CT-1992.
23-MAR-1992; 104970.
04-APR-1991; DE-110785.
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| YRLLIR 6
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Query Match

Matches

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RESULT

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Gaps

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deleted (laim 13; Page 15; 29pp; Japanese.

Claim 13; Page 15; 29pp; Japanese.

The DNA sequence from Streptococcus sobrinus strain 6715 encodes glucosyltransferase. I can mutants). The DNA was obtd. by treating 5. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA, partially digesting with saulal and fractionating on agarose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-1 expressing clone was isolated and sequenced. The clone may be used in the development of a drug for Sequence 1592 AA;
sobrinus DNA sequence with at least one nucleotide added or
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ö Gaps .; 0 Score 43; DB 6; Length 1592; Pred. No. 1.66e+02; 0; Mismatches 1; Indels Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative

371 yrllnr 376 |||| | | YRLLIR 6 g

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Search completed: Thu May 22 08:30:51 1997 Job time : 16 secs.

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I match found in sequence:
R92913; HLA-B7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913; standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).
                                                                                                                                                                                                                                                                                                          R92911 standard; peptide; 20 AA.
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2 A; 6 R; 2 N; 0 D; (
1 I; 4 L; 0 K; 0 M; (
using 'seq2' (seq2.key)
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I; 4 L; 0 K; 0 M; (
Ising 'seq2' (seq2.key)
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WPI; 95-358582/46.
                                                                                                    of the patient
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                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                         R92911;
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HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Yoptocxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      No
No
Yes
Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                    . match found in sequence:
R92909 ; HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
(from "A-GeneSeq 26")
                                                                                                                                                                                                                                                                                                                                                                                                                        'ile Options:
Indirect file
Sequence or key file
List of hits
Hit display
Name and annotations
                                                 Quest - Quick User-directed Expression Search Tool
Release 5.4
                                                                                      -- Outline of search "seq2" --
                                                                                                                                                                                                                                                                                                                                                                                                 -- Output Parameters --
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                           File
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- Run Parameters
                                                                                                                                                                                                                                                                                                                                              bank: A-GeneSeq 26, all entries
bank: PIR 50, all entries
bank: Swiss-Prot 34, all entries
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No
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Yes
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Nucleic acid code matching
Find non-matching hits only
Report key used
Note position of hit
Display full annotations
Sequence context
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Time to start comparison
Notify at end of run
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05-APR-1995; U04349.
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WPI, 95-358582/46.
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WO9526979-A1.
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Data
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class
is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MRC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 15; Page 36; 80pp; English.
R83061-R83085, R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a diner of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
CYLOCOXIC T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                 SQ 2
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                                                                                                                                                                                                                                                                                                             Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R93907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B7. These sequences can be used to extend the period of Coeptant of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inibit) the activity of the cytotoxic T lymphocytes (CTLS) of the patient.
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R83061-R83085, R83090-R83096 and R93907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate (or inibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
Lytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B7.
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                                                                                                                                                                                                                                                     Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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R92907; HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
(from "A-GeneSeq 26")
ID R92907 standard; peptide; 20 AA.
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                                                                                                                                                                                                            Krensky AM, Parham P;
                                                                                                                    12-001-1995, 004349, 05-APR-1995, U04349, 05-APR-1994; US-222851, (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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0 A; 6 R; 2 N; 0 D; 0
0 I; 4 L; 0 K; 0 M; 0
lusing 'seq2' (seq2.key)
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2 A; 6 R; 2 N; 0
                                                                                                                                                                                                          Clayberger C, Krer
WPI; 95-358582/46.
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WO9526979-A1.
             NAME OF THE PROPERTY OF THE PR
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12-NOV-1996 (first entry)
LLA-B7.84-775-84 Palindronme.
HLA, P74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; HSC70; APC;
                                                                                                                                   12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell, calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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10-NOV-1994.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
ά ϋ
                                                                         match found in sequence:
R95428; HLA-B2702 84-75-84 palindrome.
(from "A-Geneseq 26")
                                                                                                              R95428 standard; peptide; 20 AA.
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R95415 ; HLA-B7.84-75-84 Palindrome.
(from "A-GeneSeq 26")
ID R95415 standard; peptide; 20 AA
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K; 0 M; 0
(seq2.key)
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PR W9912000 AL.

18-MAY-1995, US-1500-AL.

PR 10-NOV-1994; US-150493.

A (STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM;

DR WPI; 95-140407.735.

Pr Composing lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 18; 29pp; English.

PR 55-134027.735.

Tompsons. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

PR 55-134027.735.

Tompsons. compression antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the R95413, and R95415-R95431 represent palindromes and fragments of isolate bunds last associated with T-cell lysate. P74 is a T-cell surface membrane cortaining a covalently bound with the heat shock protein HSC70.

CT 4 is found in a limited number of cell types, but is particularly coll with an amphoteric detergent, and then passed through an affinity coll with an amphoteric detergent, and then passed through an affinity coll with an amphoterising the extracellular fragment of P74 combined with the HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising the articellular fragment of P74 and determining the amount of binding between the candidate compound and p74.

CC compounds can be screened for their effect on the cytolysis. Candidate compound the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with the extracellular portion of p74, in an amount sufficient to compete the p74 for the p74 for the p74 ingand.
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
Synthetic.
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L; O K; O M; O F;
'seq2' (seq2.key)
                                                                                         W09513288-A1.
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                                 WWW.
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-- Search Statistics -Total Elapsed
00:07:13.00
Number of seminance searched.

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Number of sequences searched:

Number of sequence hits:

Number of separate matches:

Number of sequence hits saved:

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu May 22 08:48:41 1997; MasPar time 2.83 Seconds 201.600 Million cell updates/sec Run on:

Tabular output not generated. Title: Description: Perfect Score:

>US-08-653-294-31 (1-20) from US08653294.pep 154 1 YRLAIRLNERYRLAIRLNER 20 Sequence:

**PAM 150** Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 28.882; Variance 64.246; scale 0.450

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description wesult Query No. Score Match Length DB ID

Pred. No.

No matches found.

Search completed: Thu May 22 08:49:00 1997 Job time: 19 secs.

8-

US-08-653-294-31.rsp

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Thu May 22 08:48:13 1997; MasPar time 2.10 Seconds 202.262 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Tabular output not generated.

Title:

>US-08-653-294-31 (1-20) from US08653294.pep 154 1 YRLAIRLNERYRLAIRLNER 20

Description: Perfect Score: Sequence:

Scoring table:

59021 segs, 21210388 residues **PAM** 150 Gap 15 Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Mean 30.299; Variance 54.375; scale 0.557 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Result Query
No. Score Match Length DB

Pred. No.

Search completed: Thu May 22 08:48:23 1997 Job time : 10 secs.

No matches found.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 1.99 Seconds 109.404 Million cell updates/sec Thu May 22 08:49:18 1997; Run on:

Tabular output not generated.

>US-08-653-294-31 (1-20) from US08653294.pep 154 Title:

1 YRLAIRLNERYRLAIRLNER 20 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Maximum DB seq length 60

Database:

a-geneseq26
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Variance 84.009; scale 0.235 Mean 19.740;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				
Q	No. Score	Match	Match Length DB		Description	Pred. No.
٦	154	100.0	20 16		HLA-B2702 CTL modulat	
7	83			R95428	HLA-B2702 84-75-84 pa	1.33e+00
m	83			R92907	HLA-B2702 CIL modulat	1.33e+00
4	78			R92909	HLA-B2702 CTL modulat	
Ŋ	76			R92908	HLA-B2702 CTL modulat	
9	72	46.8	20		HLA-B2702 84-75T/75-8	1.09e+01
7	71				HLA-B2702 CTL modulat	1.31e+01

Note: Post-processor removed 38 summaries from list due to search parameters chosen.

# ALIGNMENTS

					MHC;
					complex;
	R92911 standard; peptide; 20 AA.		DT 16-MAY-1996 (first entry)	HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).	Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
Н	:S	1;	V-1	3270	oxic
JLT.	R9291	R92911	16-MA	HLA-E	Cytot
RESULT	a	AC	DT	DE	ΚW

And class I MHC; MLA-B2702.  Synthetic.  Synthetic.  Synthetic.  Synthetic.  We shall be shal	modulate (or inhibit) the activity of the cytotoxic r of the patient. Sequence 20 AA;  Query Match Best Local Similarity 100.0%; Score 154; DB 16; Length Matches 20; Conservative 0; Mismatches 0; Indiantic or indi	Db 1 yrlairlneryrlairlner 20 	RESULT 2  ID R95428 standard; peptide; 20 AA.  CR95428 (first entry)  DT 12-NOV-1996 (first entry)  E HLA-B2702 84-75-84 palindrome.  WW HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;  WW T-cell lysate; membrane protein; mammal; heat shock protein; HSC70; APC;  WW T-cell lysate; antigen presenting cell.  WW PC-cell lysate; antigen presenting cell.  WW D5513288-A1.  PD 18-MAX-1995.  PR NAY-1995.  PR 10-NOV-1994; UI2985.  PR 10-NOV-1993; US-150493.  PR CLAPRO JUNIV LELAND STANDORD JUNIOR.  PL CLAVBERGET C, Krensky AM.	WPI; 95-194027/25.  Tomposes. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.  Example: Page 12; 29pp; English.  Example: Page 12; 29pp; English.  RS9413, and R85415-R95431 represent palindromes and fragments of chmman-leucocyte-associated antigens. This sequence represents the chmman-leucocyte-associated antigens. This sequence represents the comman page 12; 29pp; English.  CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane of protein p74 from a T-cell lysate. p74 is a T-cell surface membrane of protein associated with real activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70.  P74 is found in a limited number of cell types, but is particularly carpsessed on B and T cells. p74 can be issolated by lysis of a suitable cell with an amphotearic detergent, and then passed through an affinity compositions comprising the extracellular fragment of p74 combined with the A-B2702 palindromic peptide.  CC oumn containing the acreened for their effect on the cytolysis. Candidate compounds and be screened for their effect on the cytolysis.  CT-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.  Modulation of CTL activity can be inhibited in a cellular composition
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Gaps

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RESULT

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75.84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS5430 standard; peptide; 20 AA.
R95430;
12-NOV-1996 (first entry)
HLA-B2702 84-75r/75-84T palindrome.
HLA-B2702 84-75r/75-84T palindrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84). Cytotoxic Tlymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient

    using Class I B75-84 MHC antigen of the recipient

                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 76; DB 16; Len
60.0%; Pred. No. 5.10e+00;
7. Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.49e+00;
1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                 50.6%; Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-1995.
05-ARR-1995.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            л 5
R92908 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 yrlairlner-renlrtalr 19
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1996 (first entry)
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les 12; Conser
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WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                        20 AA;
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                                                                                                                                                                                                                                                                                                              of the patient.
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       hosts
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         donor
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Matches
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (WHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic Tlymphocyte; CTL; major histocompatibility complex; MHC; immuosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                    Length 20;
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                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                    Score 83; DB 18; I
Pred. No. 1.33e+00;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 16; I
Pred. No. 1.33e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-ocr-1995; U04349, U5-APR-1994; U04349, U5-APR-1994; US-222851. (STRD ) UNIV LELAND STANFORD JUNIOR. Clayberger C, Krensky AM, Parham P; WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92909 standard; peptide; 20 AA.
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R92907 standard; peptide; 20
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Best Local Similarity 65.0%;
Matches 13; Conservative
                                                                                                                 h 53.9%;
Similarity 65.0%;
13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              class I MHC; HLA-B2702
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05-APR-1995; U04349.
                                                                                                                                       Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
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WO9526979-A1.
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                                                                                                                      Query Match
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NEW MARKET OF THE PROPERTY OF

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Gaps

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Indels

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Tompsons. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example 12, 29pp. English.

Example 12, 29pp. English.

RS5413, and RS5415.RS5431 represent palindromes and fragments of whan leucocyte-associated antigens. This sequence represents the HA-B2702 84-75775-847 palindrome. These sequences can be used too isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and isalso immunologically gross reactive with the heat shock protein Esc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphorteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see R95416), induces calcum influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound on the anticell and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount calcular portion of calcular portion of p74, in an amount calcular p
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell, calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
Synthetic.
WQ9513288-A1.
                                                                                                                                                                    18 MAX-1995.
10-707-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                Clayberger C, Krensky AM;
WPI; 95-194027/25.
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ij Score 72; DB 18; Length 20; Pred. No. 1.09e+01; 4; Indels 0; Mismatches h 46.8%; Similarity 72.2%; 13; Conservative 1 yrlairlnetrenlrial 18 1 YRLAIRLNE-RYRLAIRL 17 Best Local Similarity Query Match Matches 셤 ò

Gaps

HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytockoto T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702. 12-OCT-1995. 05-APR-1995; U04349. 05-APR-1994; US-222851. (STRD ) UNIV LELAND STANFORD JUNIOR. R92910 standard; peptide; 20 AA. (first entry) Synthetic. WO9526979-A1. 16-MAY-1996 RESCILA ALD BRANKWA CAN CONTROL OF THE CONTROL OF

Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R93907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of I MHC HIA-B2702. These sequences can be used to mantched donor. The peptides are administered to a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime Clayberger C, Krensky AM, Full Clayberger C, Krensky AM, Full Clayberger C, WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched form hosts - using Class I B75-84 MHC antigen of the recipient

administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient. ខ្លួន្ត

20 AA; Sequence

Gaps ä Score 71; DB 16; Length 20; Pred. No. 1.31e+01; 1; Mismatches 6; Indels 46.18; 60.08; Ouery Match
Best Local Similarity 60.0°,
12; Conservative

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Search completed: Thu May 22 08:49:27 1997 Job time: 9 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:47:21 1997; MasPar time 2.92 Seconds 195.000 Million cell updates/sec Run on:

Tabular output not generated. Title:

>US-08-653-294-26 (1-20) from US08653294.pep 154 1 YRLAIRLNERRENLRIALRY 20 Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir50

Mean 30.116; Variance 61.232; scale 0.492

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Result Query No. Score Match Length DB ID

Pred. No.

No matches found.

Search completed: Thu May 22 08:47:32 1997 Job time: 11 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:46:58 1997; MasPar time 2.04 Seconds 207.603 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-26 (1-20) from US08653294.pep 154 1 YRLAIRLNERRENLRIALRY 20 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 31.472; Variance 50.872; scale 0.619 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description ü sult Query No. Score Match Length DB Result

Pred. No.

No matches found

Search completed: Thu May 22 08:47:04 1997 Job time : 6 secs.

US-08-653-294-26.rsp

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu May 22 08:47:50 1997; MasPar time 1.97 Seconds 110.750 Million cell updates/sec Run on:

Tabular output not generated

>US-08-653-294-26 (1-20) from US08653294.pep 154 1 YRLAIRLNERRENLRIALRY 20 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 15 Scoring table:

92623 seqs, 10896596 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

a-geneseq26
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Mean 21.097; Variance 80.944; scale 0.261 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		<b>"</b> p					
Result No.	Score	Ouery Match	Query Match Length	DB	ID	Description	Pred. No.
	154	100.0	20		B95428	HIA-B2702 84-75-84 na	1 210-07
ור				) (	10000		100
7	104	T00.0	07	٩	K9.290/	HLA-B2/02 CTL modulat	1.21e-07
m	147	95.5	50	16	R92909	HLA-B2702 CTL modulat	6.09e-07
4	147	95.5	20	16	R92908	HLA-B2702 CTL modulat	6.09e-07
Ŋ	140	6.06	20	16	R92910	HLA-B2702 CTL modulat	3.05e-06
ę	131	85.1	20	18	R95430	HLA-B2702 84-751/75-8	2.39e-05
7	83	53.9	20	16	R92911	HLA-B2702 CTL modulat	9.02e-01
80	77	50.0	10	16	R83062	_	3.13e+00
σ	77	50.0	10	18	R95413	Alphal-helix of HLA-B	3.13e+00
10	77	50.0	10	ω	R41208	Peptide fragment of C	3.13e+00
11	77	50.0	15	16	R92912	HLA-B2702 CTL modulat	3.13e+00
12	77	50.0	25	18	R95422	HLAB38.6084.	3.13e+00
13	77	50.0	25	18	R95416	HLA-B2702.60-84.	3.13e+00
14	77	50.0	25	œ	R41205	Peptide fragment of C	3.13e+00
15	77	50.0	25	16	R83093	HLAB38 CTL modulating	3.13e+00
16	77	50.0	25	œ	R48286	Peptide fragment of H	3.13e+00
17	77	50.0	25	16	R83090	HLA-B2702 CTL modulat	3.13e+00
18	75	48.7	10	16	R83094	HLA-B2702 CTL modulat	4.72e+00
19	75	48.7	10	18	R95425	HLA-B2702.75-84(D).	4.72e+00

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HLA-B2702.75-84(T).	HLA-B2/02 CTL MODULAT HLA-B2702 CTL MODULAT	HLA-B7.84-75-84 Palin	HLA-B7 CTL modulating	Peptide fragment of C	HLA-B2705.75-84.	HLA-B2702 CTL modulat	HLA-B2705.60-84.	HLA-B2702 CTL modulat
R95426	R83096 R83095	R95415	R92913	R41212	R95423	R83075	R95417	R83091
18	9 7 7	18	16	ထ	18	16	18	16
25	22	50	20	10	10	10	22	25
. S. n	45.5	45.5	45.5	39.6	39.6	39.6	39.6	39.6
70	2,0	70	70	61	61	61	61	61
20	77	23	24	25	56	27	28	53

Note: Post-processor removed 16 summaries from list due to search parameters chosen.

## ALIGNMENTS

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MRC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MMC HIA-B2702. These sequences can be used to extend the period of a coeptance by a recipient of a transplant from an MMC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate (or limited period of time (compared to the lifetime modulate (or inibit) the activity of the cytotoxic T lymphocytes (CTLS) of the patient.
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R8306-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I amajor histocompatibility complex (WHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abailent for a limited period of time (compared to the lifetime administration for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CILE) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #822909; """" PEPLIGE; 20 AA.
16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; fimunosuppressant; graft versus host disorder; transplantation; therapy; Synthetic.
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graft versus host disorder; transplantation; therapy;
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                                                                                                                                                                                                                                    MHC unmatched the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayberger C, Krensky AM, Parham P;
WPI: 95-338582/46
Extension of acceptance period of transplants from
donor hosts - using Class I B75-84 MHC antigen of
                                                                                                                                                                                  05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .T 3
R92909 standard; peptide; 20 AA.
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Best Local Similarity 100.0%;
Matches 20; Conservative
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Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                 class I MHC; HLA-B2702
                                                                                                                            12-OCT-1995.
05-APR-1995; U04349.
   immunosuppressant;
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                                                                                                 WO9526979-A1.
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Gaps

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Length 20;

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Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R93907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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8381061-R83085, R81090-R83106 and R92007-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a
                                                                                                                                                                                                                                           16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant, graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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WPI; 95-358582/46.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92910 standard; peptide; 20
                                                                                                                                                                                                                 standard; peptide; 20
yrlairInerrenlrtalry 20
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05-APR-1995; U04349
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WPI; 95-358582/46.
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WO9526979-Al
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While of the proteins of the proteins of the may made in this composers. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example 12, 29pp; English.

CC R94413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequences can be used to isolate the protein associated with T-cell lysate. P74 is a T-cells surface membrane protein p74 from a T-cell lysate. P74 is a T-cells surface.

CC membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein R570.

CC modification in almitted number of cells types, but is a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HHA-B3702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60.84 (see R95416), induces calcium influx, and inhibited compounds can be screened for their effect on the cytolytic cativity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound complete with p74 for the binding of the p74, in an amount composition compete with p74 for the binding of the p74 ligand.
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HIA-B3702 84-75T/75-84T palindrome.
HIA-B3702 84-75T/75-84T palindrome.
HIA-P3702 84-75T/75-84T human-leucoyte-associated antigen; inhibitor;
HIA: p74; alphal-helix; human-leucoyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
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                                                                                                                                                                                                                                                              Score 140; DB 16; Length 20;
Pred. No. 3.05e-06;
0; Mismatches 2; Indels
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6

R05430 standard; peptide; 20 AA.

R05430; BUT-NOV-1996 (first entry)

DE HLA-B2702 84-757/75-84T palindrome.

RW HLA, p74; alphal-hellx; human-leuck

KW T-cell lysate; membrane protein; me cell; calcium influx; cytotoxic membrane protein influx; cytotoxic cell; calcium influx; cytotoxic cell; 
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Matches 18; Conser
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                                                                                                                                                    of the patient.
                                                                                                                                                                                               Sequence
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ID R9
AC R9
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HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treadmont;) The peptides particularly modulate (or inhibit) the activity of the cyctoxic T lymphocytes (CILS)
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HLA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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Sequence 10 AA;
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Immunosuppressant, graft versus host disorder, transplantation, therapy;
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor.
                                                                                                                                                                                                                                                    Example 15; Page 36; 80pp; English. R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
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                                                                                                                                                                                               MHC unmatched the recipient
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Pred. No. 3.13e+00;
...marches 0; Indels
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                                                                                                                                                                                             Extension of acceptance period of transplants from donor hosts - using Class I B75-84 MHC antigen of
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                                                                                                                                                        Parham P;
                                                                                             05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                            Clayberger C, Krensky AM,
WPI; 95-358582/46.
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Best Local Similarity 100.0%;
Matches 10; Conservative
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WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the patient.
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WO9526979-Al.
                                                             WO9526979-A1.
                          class
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Best Local S
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WPI: 95-194027/25.

Ulayberger C, Krensky AM;

WPI: 95-194027/25.

WPI: 95-194027/25.

Tomprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Tomple: Page 11; 29pp; English.

This sequence represents the alphal-helix of the fundan-leucocyte-associated antigen BDA20 (HLA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein H8c70.

P74 is found in a limited number of cell types, but is particularly capterseed on B and T cells. P74 can be isolated by 19sis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Column containing a covalently bound HLA-B2702 palindromic peptide. Column containing the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

P7-cells, by combining them with the extracellular composition containing T-cells and antigen presenting cells (APCS), by adding to the cannon of the p74 in an amount sufficient to compete cannon.
                                                                                                                                  HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; r-cell lysate; membrane protein; mammal; heat shock protein; HSc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - used for
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02-MAR-1992; U05-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
New peptide(s) based on Class I HLA antigen domains - used modulating cytotoxic T-lymphocyte activity towards targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 18; Length 10;
Pred. No. 3.13e+00;
0; Mismatches 0; Indels
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10-NOV-1993, US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R41208 standard; peptide; 10 AA.
R41208;
                                                                   .T
R95413 standard; peptide; 10
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Matches 10: Concast
                                                                                                          12-NOV-1996 (first entry) Alphal-helix of HLA-B2702.
renlrialry 10
              11 RENLRIALRY 20
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W09513288-A1.
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WO9317699-A.
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                                                                                              R95413;
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Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70.84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of The peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhbit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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HIAB38.6084.
HIAB3
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Claim 11; Page 54; 51pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
activity, either by inhibition or stimulation. It can be used
for inhibiting CTL toxicity in transplantations, for inducing CTL
activity in parasitic diseases and neoplasia and in studies on viral
infection. The peptide can also be used for identifying CTLs which
bind to it and removing subsets of CTLs from a T-cell composition.
This peptide sequence is more commonly found within larger peptide
compounds of not more than 30 amino acids in length.
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the recipient
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Pred. No. 3.13e+00;
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05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
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R92912;
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R95422;
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Best Local Similarity 100.0%;
Matches 10; Conservative
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Local Similarity 100.0%;
Local Similarity 100.0%;
Local 10; Conservative
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                                                                                                                                                                                                          Sequence
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Example: Page 9, 29pp: English.

Example: Page 9, 29pp: English.

Example: Page 9, 29pp: English.

R95413, and R94415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents than 1-1 page 1.

English 1. These sequences can be used to isolate the protein p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells.

English 2,4 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HiA-B2702 palindromic peptide.

C Compositions comprising the extracellular fragment of p74 compined with this sequence, induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can
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HLA-B2702.60-84.

HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;

T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
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Pred. No. 3.13e+00;
......+rhes 0; Indels
                                                       10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R95416 standard; peptide; 25 AA.
R95416;
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                                                                                                                 Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                     10-NOV-1994; U12985
10-NOV-1993; US-150
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                                                                                                                                          WPI; 95-194027/25.
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                                                                                                                 Clayberger C,
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be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing treells and antique presenting cells (APCS), by adding to the mix the extracellular portion of p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
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The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, antigen, or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral linfection. The peptide can also be used for inducing CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
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peptide fragment of class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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Pred. No. 3.13e+00;
0; Mismatches 0
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05-APR-1994; US-222851.
(STRD ) UNIV ELAND STANFORD JUNIOR.
FTENSKV AM, PARHAM P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1993.
25-FEB-1993; UO1758.
02-MAR-1992; UG-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R41205 standard; peptide; 25 AA.
R41205;
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                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%;
Matches 10: Concern Matches
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Best Local Similarity 100.0%;
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WPI; 95-358582/46.
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                                                                                                                                                                                                                        25 AA;
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Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of Class I major histocompatability complex (MHC) antiqees. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unnatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the sequence 25 AA;
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ö Gaps ö Score 77; DB 16; Length 25; Pred. No. 3.13e+00; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative

16 renlrialry 25 g G ŏ

Search completed: Thu May 22 08:47:56 1997 Job time : 6 secs.

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Fri May 23

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SQ 11 I; 27 L; 9 K; 5 M; 6 Found using 'seq1' (seq1.key)
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N-PSDB; Q12116.
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17-FEB-1990.

18-AGC-1988; JP-200758.

18-AGC-1989.

18-AGC-1989.

19-AGC-1989.

19-AGC-1989.

19-AGC-1989.

10-AGJ-1989.

10-AGC-1989.

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NO
Yes
Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     File Options:
Indirect file
Sequence or key file
List of hits
Hit display
Name and annotations
                                                                                                                                                                                                         Quest - Quick User-directed Expression Search Tool Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                            -- Outline of search "seg1" --
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bank: PIR 50, all entries
bank: Swiss-Prot 34, all entries
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Sequence of HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen.
EP-354580-A.
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Find non-matching hits only
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Claim 3; Page 2; 13pp; Japanese.

Probes comprising part of the DNA sequence encoding the protein can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C antigen. See also R12466 (same patent) and J03112486.
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Sequence of HLA-B51 antigen.
Probe; HLA class I DNA; immunogen.
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12465 standard; Protein; 366 AA.
12465 29-AUG-1991 (first entry)
qisktntqtyrenlrialryynqseagsht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R03144 standard; protein; 362 AA
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                                                                                                                                                                                                                                                                                                                                    1 match found in sequence:
R03144 ; Sequence of HLA-B51 antigen.
(from "A-GeneSeq 26")
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22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLIU ) OLYMPUS OPTICAL KK.
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                                                                                                                                                                                                                                                                                HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 4: Page 2: 13pp; Japanese.

Probes comprising part of the DNA sequence encoding the protein can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C antigen. See also R12465 (same patent) and J03112486
                                                                                                                                                                    All Targets (First entry)
HLA-C exon Cb-2.
HLA-C exon Cb-2.
HLA-C exon Cb-2.
HLA-C exon Cb-2.
Human leukcoyte antigen; probe; major histocompatibility complex;
Homo sapiens.
J03112485-A.
14-MAY-1991.
22-SEP-1989; JP-247695.
C2-SEP-1989; JP-247695.
(OLVU) OLYMPUS OPTICAL KK.
WPI: 91-182989/25.
N-PSDB; Q12117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-BW53 exon.
Human leukocyte antigen; probe; major histocompatibility complex;
Human sapiens.
J03112487-A.
J03112487-A.
J4-MAY-1991.
22-SEP-1999; J47697.
22-SEP-1999; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
N-PSDB; Q12114.
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R12466; HLA-C exon Cb-2.
(from "A-GeneSeq 26")
ID R12466 standard; Protein; 366 AA.
AC R12466;
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40 A; 32 R; 5 N; 20 D; 0
9 I; 30 L; 10 K; 6 M; 6
1 using 'seq1' (seq1.key)
SQ Sequence 366 AA;
SQ 38 A; 30 K; 5 N; 19 D; 0
SQ 9 I; 30 L; 10 K; 6 M; 7
Found using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   match found in sequence: R12463; HLA-Bw53 exon. (from "A-GeneSeq 26")
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14-MAY-1991.
22-SEP-1989; 247697.
22-SEP-1989; DP-247697.
22-SEP-1989; JP-247697.
22-SEP-1989; JP-247697.
WDCU ) OLYMEDS OFFICAL KK.
WPI; 91-182991/25.
N-PSDB; Q12115.
HLA-B35 gene - used in DNA probe and transformant cells for HLA-B35 gene - used in DNA probe and transformant cells for lumnishing animals, for developing monoclonal antibody.
Claim 1; Page 1; 11pp; Japanese.
Probes comprising part of the sequence encoding this sequence can be used to identify Class I genes. The DNA can be expressed for lumnisation of animals and prodn. of monoclonal antibodies specific for the HLA-B35 antigen. See also J03112485 and J03112487.
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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HLA-B35 antigen.
Human leukocyte antigen; probe; major histocompatibility complex;
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Probes comprising part of the sequence encoding the protein of used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-Bw53 antigen. See also J03112485 and J03112486.
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15 Y;
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16-SEP-1993.
25-FEB-1993.
02-YAR-1992; UG-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                       1 match found in sequence:
R12464; HLA-B35 antigen.
(from "A-GeneSeq 26")
ID R12464 standard; Protein; 362 AA.
AC R12464;
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37 A; 29 R; 6 N; 20 D; 0
12 I; 29 L; 9 K; 5 M; 7
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                                                                                           Sequence 362 AA;
38 A; 29 R; 6 N; 20
13 I; 29 L; 9 K; 6
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Homo sapiens.
J03112486-A.
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parasitic disease; cytotoxic I lymphocyte; modulation
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     respectively 16-52F-1993; U01758.

Problem 1992; US-844716.

PR (2-FB-1993; U01758.

R (2-F
           New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets modulating cytotoxic T-lymphocyte activity towards targets claim 8: Page 53; 61pp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, in paragitic of stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in paragitic diseases and neoplasta and in studies on viral infection. The peptide can also be used for identifying CTLs and to it and removing subsets of CTLs from a T-cell composition.
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
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R41206; Peptide fragment of Class I HLA peptide.
(from "A-GeneSeq 26")
ID R41206 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11207 ; Peptide fragment of Class I HLA peptide.
(from "A-GeneSeq 26")
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   Krensky AM;
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MERK B
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Clayberger CA. Krensky AM;

NPI; 93-303134/38.

RPI; 93-303134/38.

RPI; 93-303134/38.

RPI; 93-303134/38.

The weptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets

Claim 10; Page 54; 61pp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,

Claim 10; Page 54; 61pp; English.

Claim 10; Page 54; Page 55; Page 54; Page 55; Page 
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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
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Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
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R41209 ; Peptide fragment of Class I HLA peptide.
(from "A-GeneSeq 26")
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25-FBE-1993; U01758.
02-XMR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
16-SEP-1993; U01758; 25-FEB-1993; U01758; O2-MAR-1992; US-844716; (STRD ) UNIV LELAND STANFORD JUNIOR.
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R41208 standard; peptide; 10 AA.
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WPI; 93-303134/38.
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l I; 2 L; 0 K; 0 M; (
using 'seq1' (seq1.key)
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WO9317699-A.
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host
                                                                                                          Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 11; Page 54; flpp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasta and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
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WPI; 93-303134/38.

New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets
Example 13; Page 39; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
activity, ather by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide is derived from the HLA-B38 antigen and corresponds to make the amino acid positions 60-84 of that antigen.
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Peptide fragment of HLA-B38 antigen.
Human leukocyte antigen; HLA, peptide; transplantation; neoplasia;
Barasitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
W09317699-A.
                                      15-MAR-1994 (first entry)
peptide fragment of Class I HLA peptide.
Human leukocyte antigen: HLA, peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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R48286 ; Peptide fragment of HLA-B38 antigen.
(from "A-GeneSeq 26")
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25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYBEYGER CA, Krensky AM;
WPI; 93-303134/38.
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25-FEB-1993. 001758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR
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L; 1 K; 0 M; 0 F;
'seq1' (seq1.key)
standard; peptide; 10
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15-MAY-1996 (first entry)
HLA-B7 CTL modulating peptide (B7.75-84).
Cytotoxic T Lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
class I MHC; HIA-B2702.
Synthetic.
W09526979-A1.
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-E2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a
                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clayberger C, Krensky AM, Parham P;
WPI; 95-588802446.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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R83062; HIA-B2702 CTL modulating peptide (B2702.75-84).
(from "A-GeneSeq 26")
match found in sequence:
R83061 ; HLA-B7 CTL modulating peptide (B7.75-84).
(from "A-GeneSeq 26")
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12-0CT-1995.
05-ARR-1995; U04349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) FREE C, Krensky AM, Parham P;
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05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                            R83061 standard; peptide; 10
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Parham P;

STANFORD JUNIOR.

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Extension of acceptance period of transplants from MHC unmatched donor hosts • using Class I B75-84 MHC antigen of the recipient
                             Clayberger C, Kre:
WPI; 95-358582/46.
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WO9526979-A1.
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16-MAY-1996 (first entry)
16-MAY-1996 (first entry)
16-MAY-1996 (Tr. modulating peptide (B2702.70-84).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
W09528979-A1.
12-OCT-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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HLA-B7 CTL modulating peptide (B7.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B7.
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R83061-R83086, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
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      This is administered
subtherapeutic amount of an immunosuppressant. This is administere the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (of the patient.
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R92913; HLA-B7 CTL modulating peptide (B7.84-75/75-84).

(from "A-Geneseq 26")

ID R92913 standard; peptide; 20 AA.

R92913;

DT 16-MX-1996 (first entry)

DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility of munosuppressant; graft versus host disorder; transplaces synthetic.

NW 909526979-A1.

PN W09526979-A1.

PP 05-APR-1995; U04349.

PR 05-APR-1994; US-22851.
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                                                                                                                                                                                                                                                                                                                                 1 match found in sequence:
R92912 ; HLA-B2702 CTL modulating peptide (B2702.70-84).
(from "A-GeneSeq 26")
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                                                                                                              Sequence 10 AA;
1 A; 3 R; 1 N; 0 D; 0
1 I; 2 L; 0 K; 0 M; 0
| using 'seq1' (seq1.key)
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WP1; 95-358582/46.
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Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B7. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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R83061-R83085, R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an NHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration of time (compared to the lifetime administration for unrest treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-Bw46 CTL modulating peptide (Bw46.60-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-Bw46.
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R83072 ; HLA-Bw46 CTL modulating peptide (Bw46.60-84).
(from "A-GeneSeg 26")
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
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Д Б
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0 A; 6 R; 2 N; 0 D; 0
0 I; 4 L; 0 K; 0 M; 0
1 using 'seq1' (seq1.key)
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2 L; 2 K; 0 M; 0
'seq1' (seq1.key)
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05-APR-1995; U04349.
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WPI; 95-358582/46.
                                                                                                                                                                                                                                                                      of the patient.
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08:52:43 1997

Fri May 23

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HIA-B2702 CTL modulating peptide (B2702.75-84(D)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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R83094; HLA-B2702 CTL modulating peptide (B2702.75-84(D)).

(from "A-GeneSeq 26")

ID R83094 standard; peptide; 10 AA.

AC R83094;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility companimumosuppressant; graft versus host disorder; transplantt KW class I MHC; HLA-B2702.

Synthetic.

PN W05256979-A1.

PD 12-OCT-1995.
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatability complex (MRC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MRC HLA-Bw62. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MRC unnatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS) of the patient.
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R83061-R83085, R83090-R83096 and R92307-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to
                                                                                                                HLA-Bw62 CTL modulating peptide (Bw62.60-84).
Cytocovaic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-Bw62.
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HIAA-B2702 CTL modulating peptide (B2702.60-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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WPI; 95-3888EV46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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R83090 ; HLA-B2702 CTL modulating peptide (B2702.60-84).
(from "A-GeneSeq 26")
ID R83090 standard; peptide; 25 AA.
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            33073 ; HLA-Bw62 CTL modulating peptide (Bw62.60-84).
(from "A-GeneSeq 26")
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05-APR-1995; U04349.
05-APR-1994, US-222851.
(STRD ) UNV LELAND STANFORD JUNIOR.
CLAYDERGER C, Krensky AM, Parham P;
WPI; 95-358582/46.
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                      R83073 standard; peptide; 25 AA
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WO9526979-A1.
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                                                                             R83073;
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Example 13; Page 32; 80pp; English.

R83061-R83085, R8309-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MRC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for a current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
      the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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HLAB38 CTL modulating peptide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLAB38.
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Θ Η
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R83093 ; HLAB38 CTL modulating peptide (B38.6084).
(from "A-GeneSeq 26")
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WPI; 95-358582/46.
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12-OCT-1995.
05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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CC the patient for a limited proceed administration for current CC modulate (or inhibit) the a CC of the patient.
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SQ 3 A; 4 R; 1 N; 2 D; 0 SQ 2 I; 2 L; 2 K; 0 M; 0 Found using 'seq1', (seq1.key)
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found in sequence:
; HLA-B2702 CTL mo
"A-GeneSeq 26")
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WO9526979-A1.
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R92907; HLA-B
(from "A-Gene
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                                                              Example 14; Page 34; 80pp; English.

Example 14; Page 34; 80pp; English.

Example 1835 I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75.84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-R2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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16-MAY-1996 (first entry)
18-MAY-1996 or modulating peptide (B2702.75-84(L)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; Synthetic.
Synthetic.
W09526979.A1.
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05-APR-1994; US-222851.
05-APR-1994; US-222851.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                      Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host
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"A-GeneSeq 26")
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                    05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
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3 L; 0 K; 0 M; 0
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                                                              Clayberger C, Kre
WPI; 95-358582/46.
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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of Lass I major histocompatibility complex (MHC) antigens. This sequence is an inverted diner of residence 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherspeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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R83061-R83085, R83090-R833096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime
                                                                                                                                         HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; imminosuppressant; errsus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; dimunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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R92908; HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
(from "A-GeneSeq 26")
ID R92908 standard; peptide; 20 AA.
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CTL modulating peptide (B2702.84-75/75-84).
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WPI; 95-38582,42 acceptance period of transplants from MHC
Extension of acceptance period of transplants from MHC
donor hosts - using Class I B75-84 MHC antigen of the
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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05-APR-1995.
05-APR-1994; UG-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                      R92907 standard; peptide; 20
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WPI; 95-358582/46.
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Clayberger C, Krensky AM;

WPI: 95-194027/25.

Clayberger C, Krensky AM;

WPI: 95-194027/25.

Comparising lymphoid surface membrane proteins - which may compares. comprising lymphoid surface membrane protein of CTLs.

Example: Page 11: 29pp: English.

This sequence represents the alphal-helix of the man eleucocyte-associated antigen B2702 (BLA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSCTO.

P74 is found in a limited number of cell types, but is particularly captured in amphoteric detergent, and then passed through an affinity cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of P74 combined with HLA-B2702.60-84 (see R95416), induces calcum influx, and inhibits composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular composition of CTL activity can be inhibited in a cellular to compete mix the extracellular portion of P74 in an amount sufficient to compete component to the P74 ilgand.
                                                                                                                                                                                                                                                            12-NOV-1996 (first entry)
Alpha-helix of HLA-B2702.
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HLA: p74; alphal-helix; human-mammal; heat shock protein; Hsc70; APC;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic {\tt T} lymphocytes (CILs) of the patient.
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R95428; HLA-B2702 84-75-84 palindrome.

(from "A-GeneSeq 26")

ID R95428 standard; peptide; 20 AA.

AC R95428;

DT 12-NOV-1996 (first entry)

DF HLA-B2702 84-75-84 palindrome.

KW HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                        match found in sequence:
R95413 ; Alphal-helix of HLA-B2702.
(from "A-GeneSeq 26")
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        CC administration for current CC modulate (or inhibit) the CC of the patient.
SQ Sequence 20 AA,
SQ 2 A, 6 R, 2 N, 0 D, 0 SQ 1 I; 4 L, 0 K; 0 M; 0 Found using 'seq1' (seq1.key)
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Habition of CTL activity by the manner of the protein of CTL with an amploteric detergent, and Habition of CTL activity of CTL with a sequence associated antigens. This sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane controlly associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. CTL is found in a limited number of cell types, but is particularly conversed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. CC compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate CC compounds can be screened for their effect on the cytolytic activity of creening the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the companion of p74. In an amount sufficient to compete with p74 for the binding of the p74 ligand.
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calclum influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
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HLA-B2702 84-75F/75-84T palindrome.
HLA-B2702 84-75F/75-84T palindrome.
HLA-P74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composite comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example: Page 12: 29pp; English.

Example: Page 12: 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B2702 84-757/75-84T palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. p74 is found in a limited number of cell types, but is
                                                                                                                                                                                                                                                                                                                                            Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example: Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
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R95430 ; HLA-B2702 84-75T/75-84T palindrome.
(from "A-GeneSeq 26")
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                 10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
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1 L; 0 K; 0 M; (
'seq1' (seq1.key)
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WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                      Clayberger C, Kr
WPI; 95-194027/25
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                                                                                                                                                             18-MAY-1995.
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restriction of the management of the properties of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic compositions comprising the extracellular fragment of py4 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytocoxic 1ymphocyte (CTL) differentiation or cytolysis.

CC andidate compounds can be screened for their effect on the cytolytic cativity of T-cells, by combining them with the extracellular portion of py4 and determining the amount of binding between the candidate compound composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of py4.

C composition containing T-cells and antigen presenting cells (APCS), by sequence 20 AA;

S sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR 10-7807-1993; US-150493.

PR (STRO) 1993; US-150493.

RICHOWO-1994; US-150493.

I Clayberger C, Krensky AM:

WPI: 95-194027/25.

PT Compans. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

PS Example: Page 12: 29pp: English.

PS Example: Page 12: 29pp: English.

PS Example: Page 12: 29pp: English.

CC HIA-B7.60-84. These sequences can be used to isolate the protein p74 from a r-cell lysate. p74 is a T-cell surface membrane protein p74 from a rocal lycross reactive with the heat shock protein p74 from associated with r-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein p74 is containing a covalently bound HLA-B702 palindromic peptide.

C found in a limited number of cell types, but is particularly expressed on a page 12: p74 can be isolated by lysis of a suitable cell with an ampouteric detergent, and then passed through an affinity column containing a covalently bound HLA-B702 palindromic peptide.

C mopositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 condiate compound and p74.

C T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the contoint composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
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HIA-B7-60-84.
HIA-B7-60-84.
HIA-B7-60-84.
HIA-P3-760-84.
HIA-P3-760-84
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L; 2 K; 0 M; 0
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
2 A; 5 R; 2 N; 0 D; 0
2 I; 4 L; 0 K; 0 M; 0
d using 'seq1' (seq1.key)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      match found in sequence: R95431; HLA-B7.60-84.
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12-NOV-1996 (first entry)
HIA-B2702.60-84.
HIA-B2702.60-84.
HIA-PAPOZ.60-84.
HIA-PAPOZ.60-8
                                                                                                                                                                                       12-NOV-1996 (first entry)
HLA-B7.84-75-84 Palindrome.
HLA-B7.84-75-84 Palindrome.
HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytocxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
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10-NOV-1993; US-150493.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R95416; HIA-B2702.60-84.
(from "a-GeneSeq 26")
DE R95416 standard; peptide; 25 AA.
AC R95416;
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                                                                                                                               m "A-GeneSeq 26")
R95415 standard; peptide; 20 AA
                                                                                          match found in sequence: R95415; HLA-B7.84-75-84 Palindrome.
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11 20
                                                                                                                                                                                                                                                                                                               Synthetic.
W09513288-A1.
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                                                                                                                                                                         R95415;
                                                                                                                                      from
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Page 10

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qisktntqtyreslrnlrgy
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           T-cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from
           PW WOUSLEAGE AL.

PR WOUNT-1994; U12985.

PF 10-NOV-1994; U12985.

PR 10-NOV-1994; U12985.

PR 10-NOV-1994; U2-150493.

PR (STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM;

DR (STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compens. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example; Page 9; 29pp; English.

CK SP$413, and R99415-R95431 represent palindromes and fragments of thuman-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the charmon-leucocyte-associated antigens. This sequence represents the thuman-leucocyte-associated antigens. This sequence represents the number of claybration in mammalian T-cells, and is also cammunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on the amphoreric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

CC compositions compressing the extracellular fragment of P74 combined with CHA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate
                      Totaybrager V. Krensky Aw;

DR WIT: 95-194027/25.

Compsis. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Thibit cytolytic activity and differentiation of CTLs.

Example; Page 9; 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents champer-leucocyte-associated antigens. This sequence represents from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a T-cell with T-cell activation in mammalian T-cells, and is also a mambologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on mamphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the combining the mount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
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Эй
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/35.
PY Composes. Comprishing lymphoid
PT inhibit cytolytic activity and
PS Example; Page 9; 29pp; Englis
CR 895413, and 895415-R95431 reg
CC HIA-B2702.60-84. These seque
CC from a T-cell lysate. P74 is
associated with T-cell active
CC associated with T-cell active
CC found in a limited number of
CC amphoteric detergent, and the
CC compositions comprising the ecc
C compositions comprising the ecc
CC in sequence, induces calculated
CC from sequence, induces calculated
CC combining them with the extra
CC mount of binding between the
CC T-cells and antigen presenting
CC T-cells and AC 
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16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              match found in sequence:
R95418; HLA-Bw46.60-84.
(from "A-GeneSeg 26")
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While 97-19402/120.

PT Composes. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

PS Example 39, 29pp. English.

Example 39, 29pp. English.

CR 95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the CC HAL-BW62.60-84. These sequences can be used to isolate the protein p74 is a T-cell surface membrane protein p74 is a recall unannellar recells, and is also common optically cross reactive with the heat shock protein H870. Drive with an affiliality column containing a covalently bound HIA-B702 principle cell with an amphorate detergent, and then passed through an affiliality column containing a covalently bound HIA-B702 principle pptide.

Containing a covalently bound HIA-B702 palindromic peptide.

Containing the amount of the extracellular portion of p74 and determining the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
               determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition of containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 25 AA;

1 A; 5 R; 1 N; 0 B; 0 C; 3 O; 1 E; 0 Z; 1 G; 0 H;

0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA: p74; aplhal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
by combining them with the extracellular portion of p74 and
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10-NOV-1994, 1012985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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L; 1 K; 0
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WPI; 95-194027/2
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ENTRY
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 TITLE
                                                                                                                                                                                                                                                                                                       While of the properties of the proteins of CTLS.

Tompsons. comparising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 9, 29p; English.

Example: Page 9, 20p; English.

Example: Page 9, 20p; English.

Example: Page 9, 20p; English.

Example: Page 
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HIA-B2702.75-84(D).
HIA-B2702.75-84(D).
HIA. p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
T-cell ralcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                 HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
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                                                                                                                                                                                                                                           10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                          cytolysis; antigen presenting cell.
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F; 0
                  nm "A-GeneSeq 26")
R95422 standard; peptide; 25 AA.
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                                                                 12-NOV-1996 (first entry)
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L; 1 K; 0 M; 0
'seq1' (seq1.key)
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16
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R95425; HLA-B2702.75-84(D).
(from "A-GeneSeq 26")
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                                                                                                                                                                                                                    10-NOV-1994; U12985
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R95422 ; HLAB38.6084
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              from
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human-leucocyte-associated antigens.

This sequence represents the human-leucocyte-associated antigens.

This sequence represents the human-leucocyte-associated antigens.

The E2702.75-84(D). These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein cassociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on containing a covalently bound then passed through an affinity column containing a covalently bound Hzh-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with Hzh-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytocoxic Tlymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of companing them with the extracellular portion of p74 and determining the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the with p74 for the binding of the p74 ligand.

Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency and nature of errors produced in
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##note this allele is designated B*0702 (previously HLA-B7.2)
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#journal Biochemistry (1979) 18:5711-5720
#title Complete amino acid sequence of a papain-solubilized human histocompatibility antigen, HLA-B7. 2. Sequence determination and search for homologies.
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MHC class I histocompatibility antigen HLA-B7 alpha chain
precursor - human
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Proc. Natl. Acad. Sci. U.S.A. (1980) 77:1129-1133
Complete amino acid sequence of pooled papain-solubilized
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Tragardh, L.; Rask, L.; Wiman, K.; Fohlman, J.; Peterson,
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31-Jul-1980 #sequence_revision 22-Apr-1995 #text_change
06-Sep-1996
Compsns. comprising lymphoid surface membrane proteins - which may
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                            inhibit cytolytic activity and differentiation of CTLs.
Example, Page 11; 29pp, English.
R95413, and R95415-R95431 represent palindromes and fragments of
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; MHC class I histocompatibility antigen HLA-B7 alpha chain
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##residues 25-265,'E',267-295 ##label ORR
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L; 0 K; 0 M; 0
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##cross-references GDB:120048
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Found using
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REFERENCE
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107
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                                                            #accession A93840
##molecule_type protein
##molecule_type protein
##residues 25-42, 0(,44-47,'A',49-53,'N',55-68,'O',70-86,'O',88-93,
'H',95-139,'TRAI',141-175,'A',177-198,'R',200-246,'N',
248-251,'N',253-297 ##label TRA
##experimental_source pooled HLA-A, -B, and -C antigens
##note this sequence represents the predominant amino acid at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparison of a number of class I allelto sequences (*B40 vs. -B7 comparison of a number of class I allelto sequences (*B40 vs. -B7 and -B2 vs. -A28) indicates that the distribution of differences among the respective alleles (polymorphism) is essentially restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of variability between the -B40 and -B7 alleles occurs between residues 63-74. This segment and residues 147-156 are possible alloantigenic determinants of these
  -C antigens: relatedness to immunoglobulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry (1983) 22:3961-3969
Primary structure of papain-solubilized human
histocompatibility antigen HLA-B40 (-Bw60). An outline of
alloantigenic determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#domain alpha-1 #label EX1\
#domain alpha-2 #label EX2\
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MHC class I histocompatibility antigen HLA-B40 alpha chain
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#domain transmembrane #status predicted #label IMM\
#domain intracellular #status predicted #label INT\
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#formal_name Homo sapiens #common_name man
28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
                                                                                                                                                                                                                                                                                                                         #map_position 6p21.3-6p21.3

CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology

KEYWORDS duplication; glycoprotein; heterodimer; transmembrane protein; transplantation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             experimental\
3 #disulfide_bonds #status experimental
#length 362 #molecular-weight 40460 #checksum 8234
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HLHU40; MHC class I histocompatibility antigen HLA-B40 alpha chain
(from "PIR 50")
                     and internal homologies #cross-references MUID:80145722 #accession A93840
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99
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#accession A02186
HLA-A, -B, and
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A02186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Found using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                GDB: HLA-B
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307-331
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110
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GDB: HLA-B

#gene

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The seven exons correspond approximately to the domain structure of this chain.
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Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
Exon/intron organization and complete nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain signal sequence #status predicted #label SIGN
#product class I histocompatibility antigen HLA alpha
chain #status predicted #label MATN
#domain extracellular #status predicted #label EXTN
#domain alpha-1 #label EX1N
#domain alpha-2 #label EX2N
#domain immunoglobulin homology #label IMMN
#map_position 6p21.3-6p21.3

CLASSIFICATION #superfamily class I histocompatibility antigen;
Immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; membrane protein;
transplantation antigen
                                                                                                                                                                                                    #domain alpha-1 #label EXI\
#domain alpha-2 #label EXZ\
#domain immunoglobulin homology #label IMM\
#bluding_site carbohydrate (Asn) (covalent) #status
experimental\
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted\
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immunoglobulin homology
duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
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#length 359 #molecular-weight 40548 #checksum 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 match found in sequence:
HLHU12; MHC class I histocompatibility antigen HLA alpha chain
(from "PIR 50")
                                                                                                                                                                                                                                                                                                                                                                    8 #disulfide_bonds #status predicted
#length 270 #checksum 4804
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#cross-references MUID:82151002
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#accession
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Found using
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Found using
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#authors
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SUMMARY
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DATE
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                                                                                                                                                                                                                                                                                                                                                        #authors Sodoyer, R.; Damotte, M.; Delovitch, T.L.; Trucy, J.; Jordan, B.R.; Strachan, T.
#journal BMBO J. (1984) 3:879-885
#title Complete nucleotide sequence of a gene encoding a functional human class I histocompatibility antigen (HLA-CW3).
#accession A02190
                                                                                                                                                    HILHUW3 #type complete
MHC class I histocompatibility antigen HLA-Cw3 alpha chain
precursor - human
#formal_name Homo sapiens #common_name man
04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
A02190
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MHC class I histocompatibility antigen HLA-C4 alpha chain
human
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
A24512
A92500
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protein; transplantation antigen
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th 366 #molecular-weight 40744 #checksum 4249
                                                                                                                                           LHUW3; MHC class I histocompatibility antigen HLA-Cw3 alpha chain (from "PIR 50")
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HLHUC4 ; MHC class I histocompatibility antigen HLA-C4 alpha chain
(from "PIR 50")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #ETICS
#gene GDB:HLA-C
#secoss-references GDB:119311
##ap_position 6p21.3-6p21.3
#introns 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
#introns 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
#introns assistication #superfamily class I histocompatibility antigen;
immunoqlobulin homology
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96 105
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108
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                                                                                                                              1 match found in sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION
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220-285
308-332
333-366
110
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      86
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ERENCE A26088

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A26088
#authors Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
#journal J. Blol. Chem. (1985) 260:13414_13423
#title Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and HLA-C genes.
#cross-references MUID:86033791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLHU32 #type fragment
MHC class I histocompatibility antigen HLA-A32 alpha chain
human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name_Homo_sapiens #common_name_man
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
A26088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain immunoglobulin homology #label IMM #length 342 #molecular-weight 38082 #checksum 7418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      match found in sequence:
HLHU32 ; MHC class I histocompatibility antigen HLA-A32 alpha chain
(from "PIR 50")
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#gene
#gene
#gene
##cross-references GDB:119310
##map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS glycoprotein; heterodimer; transmembrane protein;
transplantation antigen
                                                                                                                                                                                                                                                      GENETICS
GDB:HLA-C
##cross-references GDB:119311
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
Immunoglobulin homology
KEYWORDS glycoprotein; heterodimer; transmembrane protein;
transplantation antigen
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th 274 #checksum 899
                                                                                                                             #cross-reterencccssion A24512
#accession A24512
##molecule_type DNA
1-342 ##label DAV
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##residues 1-274 ##label WAN
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75
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75 84
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HIAUDB #type complete
MHC class I histocompatibility antigen HLA-Bw58 alpha chain
precursor - human #formal_name Homo sapiens #common_name man
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                        1-362 ##label WAY the authors translated the codon GCC for residue 349 as the authors translated the codon \ensuremath{\mathsf{GCC}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIMSDB #type complete
MHC class I histocompatibility antigen H-2D(b) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain signal sequence *status predicted #label SIGN *product class I histocompatibility antigen HLA-Bw58 alpha chain #status predicted #label MATN #domain extracellular *status predicted #label EXTN #domain alpha-1 #label EXIN #domain alpha-2 #label EXIN #domain immunoglobulin homology #label IMMN #domain immunoglobulin homology #label IMMN #domain intracellular *status predicted #label IMMN #domain intracellular *status predicted #label IMMN #domain intracellular *status predicted #label IMMN #domain #label IMMN #domain intracellular *status predicted #label INT #length 362 #molecular-weight 40321 #checksum 8057
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Immunogenetics (1982) 16:1-9
The complete amino acid sequence of the murine
transplantation antigen H-2D(b) as deduced by molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Mus musculus #common_name house mouse
29-Jul-1981 #sequence_revision 14-Nov-1983 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found in sequence:
; MHC class I histocompatibility antigen HLA-Bw58 alpha chain
"PIR 50")
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HIMSDB ; MHC class I histocompatibility antigen H-2D(b) alpha chain
(from "PIR 50")
                                                                                                                                                    #journal Ways, J.P.; Coppin, H.L.; Parham, P. #journal J. Biol. Chem. (1985) 260:11924-11933 #title The complete primary structure of HLA-Bw58. #accession A23895 #fmolecule_type DNA ##rolecule_type DNA ##rolecule_type DNA ##rolecule_type DNA ##rolecule.
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This protein is a subtype of the HLA-B17 family
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#cross-references MUID:83005712
#accession A91747
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#title
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duplication; glycoprotein; heterodimer; transmembrane protein
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                                                                                                                                                                                                                                                                                                        #authors Maloy, W.L.; Coligan, J.E.
#journal Immunogenetics (1982) 16:11-22
#title Primary structure of the H-2D(b) alloantigen. II. Additional anino acid sequence information, localization of a third site of glycosylation and evidence for K and D region #cross-references MUID:83005713
#accession A91748
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Structural relationships among the H-2 D-regions of murine
MHC haplotypes.
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#disulfide_bonds #status predicted\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 338 #molecular-weight 38402 #checksum 4501
                                                      #authors Maloy, W.L.; Nathenson, S.G.; Coligan, J.E.
#journal J. Biol. Chem. (1981) 256:2863-2872
#title Primary structure of murine major histocompatibility compalities.
#long alloantigens. Amino acid sequence of the NH-2-terminal ninety-eight residues of the H-wD(b) glycoprotein.
#cross-references MUID:81142266
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#domain alpha-2 #label EXI\
#domain immunoglobulin homology #label IMM\
#domain iransmembrane #status predicted #label IMM\
#domain intracellular #status predicted #label IMM\
#domain intracellular #status predicted #label INM\
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#formal_name Mus musculus #common_name house mouse
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
12-Apr-1995
A30547
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A30547 ; class I histocompatibility antigen H-2D-b alpha chain - mouse
(from "PIR 50")
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#superfamily class I histocompatibility antigen;
Immunoglobulin homology
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##residues 1-206 ##label DUR
##residues 1-206 ##label DUR
##rearioN #superfamily class I histocompatibility antigen;
immunoglobulin homology
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##molecule_type protein
##residues 229-284;308-332,'X',334 ##label MA2
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1-338 ##label REY
A9<u>2</u>315
                                                                                                                                                                                                                             ##molecule_type protein
##residues 1-98 ##label MA1
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176
               ##residues
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1-83
1-83
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91-182
196-261
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86 7-8
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##residues
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299-338
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25-363
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$03537
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S03538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A35997 #type complete
MHC class I histocompatibility antigen HLA-A25 alpha chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Falk, K.; Rotzschke, O.; Grahovac, B.; Schendel, D.; Stauthors Stevanovic, S.; Gnau, V.; Jung, G.; Strominger, J.L.; Rammensee, H.G. **

#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:12005-12009 #title Allele-specific peptide ligand motifs of HLA-C molecules. #cross-references MUID:94089758
                                                                                                                                                                                                                                                                                    A49411 #type fragment
human leukocyte anitgen, HLA-C (alpha 1 and 2 domains)
human (fragment)
#formal_name Homo sapiens #common_name man
07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor - human
#formal_name Homo sapiens #common_name man
16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change
26-Apr-1996
A35997
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A3597; MHC class I histocompatibility antigen HLA-A25 alpha chain
(from "PIR 50")
A35997 #type complete
ENTRY MHC class I histocompatibility antigen HLA-A25 alp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence extracted from NCBI backbone
#superfamily class I histocompatibility antigen;
immunoglobulin homology
#length 182 #checkeum 3873
                                                                                                                                                                                                             l match found in sequence:
A49411; human leukocyte anitgen, HLA-C (alpha 1 and 2 domains)
(from "PIR 50")
ENTRY
 #checksum 9521
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##residues 1-182 ##label FAL
##cross-references NCBHP:141047
##experimental_source CIR cell line
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75 84
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#length 206
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#authors Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer,
G.; Klein, J.
#journal EMBO 7. (1988) 7.2755-2774
#title Nucleotide sequences of chimpanzee MHC class I alleles:
    evidence for trans-species mode of evolution.
#cross-references MUID:89030641
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#product class I histocompatibility antigen alpha chain
#label MAT\
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class I histocompatibility antigen Chia-Bl alpha chain
precursor - chimpanzee
#formal_name Pan troglodytes #common_name chimpanzee
18-oct-1989 #sequence_revision 18-oct-1989 #text_change
$03537
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class I histocompatibility antigen ChLA-B2 alpha chain
precursor - chimpanzee (fragment)
#formal_name Pan troqlodytes #common_name chimpanzee
18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
50-Apr-1996
                                                                                                                  #domain immunoglobulin homology #label IMM #length 364 #molecular-weight 41147 #checksum 1931
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CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
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#domain immunoglobulin homology #label IMM\
#domain transmembrane #label TMM\
#domain intracellular #label INI
rth 363 #molecular-weight 40633 #checksum :
##cross-references GB:M32321
FICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
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    class I histocompatibility antigen ChLA-B2 alpha chain
    "PIR 50")
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##residues 1-363 ##label_MAY
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66

REFERENCE

##note

216-281 295-333 334-358

SEQUENCE

82

SUMMARY

21-294

KEYWORDS FEATURE 1-20 21-358

```
#domain signal sequence #label SIG\
#product class I histocompatibility antigen heavy chain,
Gogo-B0103 #status predicted #label CLA\
#domain alpha-1 #label AL1\
#domain alpha-2 #label AL2\
#domain inmunoglobulin homology #label IMM\
#domain inmunoglobulin homology #label IMM\
#domain intracellular #label INT
#length 362 #molecular-weight 40248 #checksum 7416
                                                                                                                                                                               JH0541 #type complete class I histocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla #formal_name Gorilla gorilla gorilla gorilla gorilla
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#journal J. Exp. Med. (1991) 174:1491-1509
#title Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I.
#cross.references MUID:92078860
#accession JH0539
##molecule_type DNA
##residues 1-362 ##label LAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P. J. Exp. Med. (1991) 174:1491-1509 Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.
                                                                                                                                                                                                                                                                                                                                                 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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JH0541; class I histocompatibility antigen Gogo-B0103 heavy chain
(from "PIR 50")
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JH0539 ; class I histocompatibility antigen Gogo-B0101 heavy chain
(from "PIR 50")
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#superfamily class I histocompatibility antigen;
immunoglobulin homology
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99
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#accession JH0541
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CLASSIFICATION
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#title
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115-206
207-298
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299-362
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25-362
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#journal J. Immunol. (1989) 142:306-311
#title HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha-1 domain.
#cross-references WID:89080265
#accession B30345
#authors Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, G.; Klein, J.
#journal EMBO J. (1988) 7:2765-2774
#title Nucleotide sequences of chimpanzee MHC class I alleles:
evidence for trans-species mode of evolution.
#cross-references MUD:89030641
#accession S03538
                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-358 ##label MAY
##cross-references EMBL:X13116
##cross-references EMBL:X13116
##note the four residues preceding 1-Ala shown in Fig. 6 were
##note apparently misplaced from the sequence of the ChLA-Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain signal sequence (fragment) #label SIG\
#product class I histocompatibility antigen alpha chain
#label MAT\
                                                                                                                                                                                                                                                                                                                                                    protein
the authors translated the codon CCG for residue 125 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B30345 #type complete
MHC class I histocompatibility antigen HLA-Bw52 precursor
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29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
26-Apr-1996
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B30345; MHC class I histocompatibility antigen HLA-Bw52 precursor
(from "PIR 50")
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#domain immunoglobulin homology #label IMM\
#domain transmembrane #label IMM\
#domain intracellular #label INT
#length 358 #checksum 1496
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immunoglobulin homology
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#superfamily class I histocompatibility antigen;
immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein
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##residues
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220-285 SUMMARY

SEQUENCE

83

ACCESSIONS REFERENCE

ORGANISM

DATE

TITLE

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##residues
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#description
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ENTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                             #product class I histocompatibility antigen heavy chain, Gogo-B0101 #status preditted #label CLA\
#domain alpha-1 #label AL1\
#domain alpha-2 #label AL2\
#domain alpha-3 #label AL3\
#domain imminoglobulin homology #label IMM\
#domain intracellular #label INT
#length 362 #molecular #label INT
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#product class I histocompatibility antigen heavy chain,
Gogo-B0102 #status predicted #label CLA\
#domain alpha-1 #label AL1\
#domain alpha-2 #label AL2\
#domain alpha-3 #label AL3\
#domain immunoglobulin homology #label IMM\
#domain intracellular #label INT
#length 362 #molecular-weight 40204 #checksum 7312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JH0540 #type complete
class I histocompatibility antigen Gogo-B0102 heavy chain
precursor - lowland gorilla
#formal_name Gorilla gorilla gorilla
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
JH0540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal J. Exp. Med. (1991) 174:1491-1509
#title Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I.
#cross-references WIUD:92078860
#accession JH0540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; class I histocompatibility antigen Gogo-B0102 heavy chain "PIR 50")
                                                  25/1; 115/1; 207/1; 299/1; 338/1; 349/1
#superfamily class I histocompatibility antigen;
immunoglobulin homology
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#superfamily class I histocompatibility antigen;
immunoglobulin homology
                                                                                                                             #domain signal sequence #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-362 ##label LAW
##cross-references EMBL:X60693
##experimental_source EBV-transformed B cell
                   ##experimental_source EBV-transformed B cell
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99 108
##cross-references EMBL:X60255
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                                                      #introns
CLASSIFICATION
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SUMMARY
SEQUENCE
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115-206
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299-362
SUMMARY
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25-362
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                                   GENETICS
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(from "
ENTRY
TITLE
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S16789
S16786
Madrigul, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.; Petzl-Erler, M.L.; Martell, R.W.; Du Toit, E.D.; Parham, P. Submitted to the EMBL Data Library, August 1991
Molecular definition of HiA-A,B antigens of black populations: Implications for HIA matching and typing in complex HLA-C alpha chain #formal\_name Homo sapiens #common\_name man 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 26-Apr-1996 849381 S16789 #type complete class I histocompatibility antigen HLA-Bw72 alpha chain human #formal\_name Homo sapiens #common\_name man 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 06-Sep-1996 #domain immunoglobulin homology #label IMM #length 366 #molecular-weight 40915 #checksum 4194 #domain immunoglobulin homology #label IMM #length 362 #molecular-weight 40387 #checksum 408 found in sequence: ; class I major histocompatibility complex HLA-C alpha chain "PIR 50") S49381 Pablo, R. submitted to the EMBL Data Library, October 1994 S49381 ##Cross-references EMBL:X82122 CLASSIFICATION #superfamily class I histocompatibility antigen; immunoglobulin homology GENELICO
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#10 match found in sequence: 16789 ; class I histocompatibility antigen HLA-Bw72 alpha chain (from "PIR 50") S49381 #type complete class I major histocompatibility 1-366 ##label PAB 1-362 ##label MAD qkykrqaqadrvslrnlrgyynqseagsht 99 108 ##cross-references EMBL:X61709 transplantation preliminary SEQUENCE Found using 'seq1' (seq1.key) SEQUENCE Found using 'seq1' (seq1.key) #accession S16789 ##molecule\_type mRNA ##molecule\_type mRNA human 220-285 SUMMARY

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qtskaqaqtdrenlrialryynqseagsht

8

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SEQUENCE
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                                                                                                                                                                                                            128 #type complete class I histocompatibility antigen HLA-C precursor (clone
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ш
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Three new class I HLA alleles: structure of mRNAs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A45880 #type complete
MRC class I histocompatibility antigen HLA-B35 alpha chain
precursor - human
#formal_name Homo sapiens #common_name man
03.Jun-1993 #sequence_revision 03.Jun-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ooba, T.; Hayashi, H.; Karaki, S.; Tanabe, M.; Kano, K.; Takiguchi, M.
Immunogenetics (1989) 30:76-80
Instructure of HLA-B35 suggests that it is derived from HLA-Bw58 by two genetic mechanisms.
                                                                                                                                                                                                                                                #formal_name Homo sapiens #common_name man
14-Feb-1992 #sequence_revision 03-Apr-1992 #text_change
06-Sep-1996
B37028
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B37028 ; MHC class I histocompatibility antigen HLA-C precursor (clone
(from "PIR 50")
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th 366 #molecular-weight 40884 #checksum 6126
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##cross-references GB:M28109; GB:M28111; GB:M28112;
GB:M28113; GB:M28114; GB:M28115
##note this allele is designated B*3501
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A45880 ; MHC class I histocompatibility antigen HLA-B35 alpha chain
(from "PIR 50")
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#gene #gene #gene #feross-references GDB:119311
##cross-references GDB:119311
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                    alternative mechanisms of processing.
#accession B37028
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##cross-references GB:M24097
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A45880; S32754; S32755
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10) - human
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B.; Ziegler, A.; Schendel, D.J.
submitted to the EMBL Data Library, April 1993
Natural microheterogeneity in HIA-B35 alleles influences
peptide-dependent allorecognition by cytocoxic r cells but
not of a peptide-restricted monoclonal antibody.
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Proc. Natl. Acad. Sci. U.S.A. (1990) 87:833-2833.
Rapid cloning of HLA-A.B CDNA by using the polymerase chain
reaction: frequency and nature of errors produced in
Steinle, A.; Reinhardt, C.; Noessner, E.; Uchanska-Ziegler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D35997 #type complete
MHC class I histocompatibility antigen HLA-B57 alpha chain
precursor - human
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#domain immunoglobulin homology #label IMM
#length 362 #molecular-weight 40455 #checksum 285
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Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Homo sapiens #common_name man
16.Nov-1990 #sequence_revision 13-Jan-1993 #text_change
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D35997; MHC class I histocompatibility antigen HLA-B57 alpha chain
(from "PIR 50")
ENTRY #type complete
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#GDB:HLA-B
#gene #cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
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#journal Nucleic Acids Res. (1990) 18:6702
Wiltitle Nucleotide sequence of an HLA-Bw57 gene.
#cross-references MUID:91067476
                                                                                                                      ##cross-references GB:M32318
##note this allele is designated B*5701
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##note this allele is designated B*5701
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##residues 1-179,'R',181-362 ##label ST2
##cross-references EMBL:Z22643
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##residues 1-364 ##label ENN
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D35997; S12622; S16774
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#cross-references MUID:90207291
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08:52:43 1997

23

Fri May

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Allospecificities between HIA-BW53 and HIA-B35 are generated by substitution of the residues associated with HIA-BW4/BW6
R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.; Petzl-Erler, M.L.; Martell, R.W.; Du Toit, E.D.; Parham, P. submitted to the EMBL Data Library, August 1991 Molecular definition of HLA-A,B antigens of black populations: Implications for HLA matching and typing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.;
Takiguchi, M.
Immunogenetics (1990) 32:195-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A45834  #type complete
MHC class I histocompatibility antigen HLA-B53 alpha chain
precursor - human
#formal_name Homo sapiens #common_name man
03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
06-Sep-1996
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#domain immunoglobulin homology #label IMM\
#binding site carbohydrate (Asn) (covalent) #status
predicted
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#domain immunoglobulin homology #label IMM
#length 364 #molecular-weight 40451 #checksum 386
                                                                                                                                                                                         duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
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A45834 ; MHC class I histocompatibility antigen HLA-B53 alpha chain
(from "PIR 50")
BNTRY A45834 #type complete
                                                                                                                                                                                                                                                                                   #gene GDB:HLA-B
##cross_references GDB:120048
#map_position 6p21.3-6p21.3
#introns 25/2; 115/1; 207/1; 299/1; 338/1; 349/1
#SSIFICATION #superfamily class I histocompatibility antigen; immunoglobulin homology
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immunoglobulin homology
heterodimer; transmembrane protein
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##cross-references GB:M58636; GB:M33574
##note this allele is designated B*5301
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##cross-references GDB:120048
#map_position 6p21.3-6p21.3
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#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L. Nature (1992) 357:329-333 #title Nature (1992) 357:329-333 #title New recombinant HiA-B alleles in a tribe of South American American andicate rapid evolution of MHC class I loci. #cross-references MUID:92269956
                                                                                                                                                                                                                                               Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L. Nature (1992) 357:329-333
                                                                                                                                                                                                                                                                                                                          #title New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.
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; class I histocompatibility antigen - human
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1 match found in S24434 ; class I
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New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.
                                                                                                                                                                                                                       $24027  #type complete class I histocompatibility antigen - human formal_name Homo saplens #common_name man 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Apr-1996
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class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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S24437 ; class I histocompatibility antigen - human
(from "PIR 50")
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91
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95 104
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#authors S24027
#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; #journal S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L. hybornal New recombinant HiA-B alleles in a tribe of South American #merindians indicate rapid evolution of MHC class I loci.#cross-references MUID:92269956
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#formal_name Homo sapiens #common_name man
22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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#molecular-weight 39403 #checksum 5245
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#length 354
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Found using 'seq1' (seq1.key)
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##residues 1-35
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#domain immunoglobulin homology #label IMM

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##residues
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$24439 ; class 1
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S24436 #type complete

Class I histocompatibility antigen - human

SANISM #class I histocompatibility antigen - human

22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change

26-Apr-1996

S24037

S24037

BLI: McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; Ghim, S.H.; Troup, G.W.; Hughes, A.L.; Letvin, N.L.

#journal New recombinant HLA-B alleles in a tribe of South American

#cross-references MUID:9269956
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#title New recomplinant HiA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.
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#length 362 #molecular-weight 40462 #checksum 9855
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##residues 1-362 ##label WAT
FICATION #superfamily immunoglobulin homology
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S24435 ; class I histocompatibility antigen - human
(from "PIR 50")
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S24436 ; class I histocompatibility antigen - human
(from "PIR 50")
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#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.; Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L. afjournal Nature (1992) 357:329-333
#title New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci. #cross-references MUID:92269956
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#title Distinctive HLA-A,B antigens of black populations formed by interalialic conversion.
#cross-references MUID:93056508
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MHC class I histocompatibility antigen HLA-B45 alpha chain
precursor - human
precursor - human
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
06-Sep-1996
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class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
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th 274 #molecular-weight 31614 #checksum 836
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137519 ; MHC class I histocompatibility antigen HLA-B45 alpha chain
(from "PIR 50")
preliminary; translated from GB/EMBL/DDBJ
#domain immunoglobulin homology #label
#length 362 #molecular-weight 40396 #check
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24439 ; class I histocompatibility antigen - human
(from "PIR 50")
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##residues 1-362 ##label RES
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                                                                               'seq1' (seq1.key)
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GENETICS

1-24 220-285 110

FEATURE

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qifktntqtdreslrnlrgyyngseagsht
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##cross-references GDB:120048
                                                                                                                                                 137522; $16775
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##molecule_type DNA
##residues 1-36
        (from "PIR 50")
                                                                                                                                                                                                                                                                                                                                                            ##status
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SUMMARY
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172113 ;
(from "
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MHC class I histocompatibility antigen HLA-Bw50 alpha chain
precursor - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.; Petzl-Erler, M.L.; Du Tolti, E.D.; Parham, P.
J. Immunol. (1992) 149:3411-3415
Distinctive HLA-A,B antigens of black populations formed by
                                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#domain immunoglobulin homology #label IMM\
#binding_site carbohydrate (Asn) (covalent) #status
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37520 ; MHC class I histocompatibility antigen HLA-Bw50 alpha chain
(from "PIR 50")
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                                                                                                                                                                                                                                                                                              #length 362 #molecular-weight 40414 #checksum 56
                                                         #gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3 6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS heterodimer; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GDB:HLA-B##cross-references GDB:120048##cross-references GDB:120048#map_position 6p21.3-6p21.3

CLASSIFICATION #superfamily class I histocompatibility antigen; immunoglobulin homology
##cross-references EMBL:X61710; NID:932182; CDS_PID:932183
##note this allele is designated D*4501
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137520; S16773
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SEQUENCE
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#title
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#authors

ACCESSIONS REFERENCE

ORGANISM

TITLE

match 1 137520

89

220-285

SUMMARY

83

GENETICS

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#authors Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.; # Petzl-Erler, M.L.; Du Tolt, E.D.; Parham, P. J. Immunol. (192) 149:3411-3415 #title Distinctive HLA-A,B antigens of black populations formed by #cross-references MuID:93056508 #accession 137522
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137522 #type complete
MHC class I histocompatibility antigen HLA-Bw78 alpha chain
                                                                precursor - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
06-Sep-1996
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histocompatibility antigen HLA-C alpha chain (allele Cw 12022) precursor antigen HCA-C alpha chain (allele Cw 12022) precursor sapiens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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"ERENCE 156034

#authors 156044, M.; Nishimura, I.; Hayashi, H.; Karakl, S.;

#fournal Tamunol. (1989) 143:1372-1378

#title The structure and expression of genes encoding serologi undetected HLA-C locus antigens.

#cross-references MUID:89309827

#accession 172113
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CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references EMBL:X61708; NID:g32190; CDS_PID:g32191
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    histocompatibility antigen HLA-C alpha chain (allele Cw
    "PIR 50")
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##molecule_type_nRNA
##residues-1-366 ##label VIL
##cross_references EMBL:X70856
##note
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CLASSIFICATION
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#journal
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ENTRY
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                                                                                                                     DATE
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#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HIA-B51 and HIA-B52 differ by only two amino acids which are in the helical region of the alpha-1 domain.
#cross-references MIID:89080265
                                                                                                                                                                                                                                                                                                                                                                                A30345 #type complete
MHC class I histocompatibility antigen HLA-B51 precursor
human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Homo sapiens #common_name man
29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
06-Sep-1996
$31345; IS8746
                                                                                                    #label IMM
#checksum 4159
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#title Allelic variation in HLA-B and HLA-C sequences and evolution of the HLA-B alleles.
#cross-references MUID:89233295
                                                                                                                                                                                                                                                                                                                 I match found in sequence:
A30345; MHC class I histocompatibility antigen HLA-B51 precursor
(from "PIR 50") A3033R
GENEILLS

#gene
#gene
#gene
#scross-references GDB:120048
#map_position 6p21.3-6p21.3

#map_position fsuperfamily class I histocompatibility antigen;
immunoglobulin homology
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##residues 1-362 ##label RES
##cross-references GB:L41087; NID:9735900; CDS_PID:9735902
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                                                                                                    #domain immunoglobulin homology #length 366 #molecular-weight 40885
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##rps://or
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#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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                                                                                                                                                                                    S25536 #type complete
MHC class I histocompatibility antigen - rat
#formal_name Rattus norvegicus #common_name Norway rat
20.Feb-1995 #sequence_revision 20.Feb-1995 #text_change
06-Sep-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Rothermel, E.; Heine, L.; Wurst, W.; Gunther, E.
#journal Immunogenetics (1993) 38:82-91
#title Characterization of a class Ib gene of the rat major histocompatibility complex.
#cross-references MID:93246303
#accession 183469
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T #Length 354 #checksum 3211
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##residues 1-353 ##label RES
##cross-references EMBL:X67504; NID:956484; CDS_PID:956485
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##molecule_type mRNA
##residues 1-354 ##label RES
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; class I histocompatibility antigen – pygmy chimpanzee
"PIR 50")
found in sequence:
. MHC class I histocompatibility antigen - rat
"PIR 50")
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91
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I83469; S25536
I60327
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                                                                                                                                                                                                                                                                 #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#tille Aunguley high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references WIDI:94286544
#accession 180166
                                                                                                                      (fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
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                                                                           180165 #type fragment
class I histocompatibility antigen - pygmy chimpanzee
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class I histocompatibility antigen – pygmy chimpanzee
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##cross-references EMDL:U05577; NID:9454771; CDS_PID:9454772
:X #length 354 #checksum 3443
                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1354 ##label RES ##cross-references EMBL:U05576; NID:9454769; CDS_PID:9454770 ** #length 354 #checksum 2453
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##molecule_type mRNA
###nceid...
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##molecule_type mRNA
##psidin...
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180165 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY 180165 #tvpe fragment
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180167 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
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180166 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
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#type fragment class I histocompatibility antigen - chimpanzee (fragment) #formal_name Pan troglodytes #common_name chimpanzee 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-May-1996
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ANISM #tormal_lane Pan troglodytes #common_name (fragment)

ANISM #formal_lane Pan troglodytes #common_name chimpanzee

24-May-1996 #sequence_revision 24-May-1996 #text_change

24-May-1996

ESSIONS 189168

ESSIONS 159308

NoAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897

# title A uniquely high level of recombination at the HLA-B locus.
                                                                                                                                                                                                                     #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
# title A uniquely high level of recombination at the HIA-B locus. #accession 180167
                                                    (fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
                                                                                                                             24-May-1996 #sequence_revision 24-May-1996 #text_change
180167  #type fragment
class I histocompatibility antigen - pygmy chimpanzee
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180169; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
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180168 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-354 ##label RES
##cross-references EMBL:U05579; NID:9454775; CDS_PID:9454776
Y #length 354 #checksum 5067
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Found using 'seq1' (seq1.key)
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##residues 1-35
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class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
180175
PERSIONS 180169
FREENCE 159308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
A uniquely high level of recombination at the HLA-B locus. #cross-references MID:94286544
#accession 180169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Warkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
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180175 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
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                                                                                                                                                                        ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA ##rosidues 1.355 ##label RES ##cross-references EMBL:U05580; NID:9454777; CDS_PID:9454778 XY #length 355 #checksum 4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:U05582; NID:9454781; CDS_PID:9454782
Y #length 355 #checksum 6021
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##molecule_type mRNA
##residues 1-355 ##label RES
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180171 ; class I histocomp
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ENTRY 180171
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136957 #type complete
MHC ChlA chain - chimpanzee
#formal_name Pan troglodytes #common_name chimpanzee
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
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MHC ChlA chain - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
02-ul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
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##cross-references GB:M24045; NID:g176814; CDS_PID:g176815
Y #length 363 #molecular-weight 40540 #checksum 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. #journal J. Immunol. (1989) 142:3937-3950 #title Diversity and diversification of HLA-A,B,C alleles.#cross_references_MUID:89235215
                                                                                                 ##cross_references EMBL:U05586; NID:q454789; CDS_PID:g454790 Y #length 137 #checksum 5336
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##molecule_type mRNA
##residues 1-308 ##label RES
##cross-references GB:MZ4044; NID:9176812; CDS_PID:9176813
XY #length 308 #checksum 7529
##status preliminary; translated from GB/EMBL/DDBJ##molecule_type mRNA ##modians
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##molecule_type mRNA
##presidin...
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136956; MHC ChlA Chain - chimpanzee (fragment)
(from "PIR 50") 136956 #type fragment
                                                                     1-137 ##label RES
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ACCESSIONS REFERENCE

SEQUENCE

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SUMMARY

ORGANISM

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"BRENCE 154298 Chertkoff, L.P.; Herrera, M.; Fainboim, L.; Satz, M.L.
Authors Chertkoff, L.P.; Herrera, M.; Fainboim, L.; Satz, M.L.
#journal Hum. Immunol, (1991) 31:153-158
#title Complete nucleotide sequence of a genomic clone encoding
#title HA-B35 isolated from a Caucasian individual of Hispanic
Origin. Identification of a new variant of HLA-B35.
#cross-references MUID:91365651
                                                                                                                                                                                                                #authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162045 #type complete
gene HLA B-1517 protein - human
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene name HLA B-1517
#length 362 #molecular-weight 40417 #checksum 7730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *length 362 *molecular-weight 40564 *checksum 567
                                                                                                                                                                                                                                                                                                                                                                                                           ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues
##cross-references EMBL:U01848; NID:g402676; CDS_PID:g402677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #residues 1.362 ##label RES
#cross-references GB:M63454; NID:g187856; CDS_PID:g403145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues
##residues
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match found in sequence:
162045 ; gene HLA B-1517 protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rnmkasaqtyrenlrialryynqseagsht
99 108
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| q1fktntqtyreslrnlrgyyngseagsh1
| 99
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154298 ; gene HLA-B protein - human
(from "PIR 50")
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SEQUENCE
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                             62045 ; gene HL
(from "PIR 50")
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#authors
#journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics (1984) 20:237-252
Inter-locus and intra-allelic polymorphisms of HLA class I
                                                                                                                                                                           130958 #type fragment
MHC ChlA chain - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
02.Jul-1996 #sequence_revision 02.Jul-1996 #text_change
136958
136956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168701 #type fragment
cell surface antigen - human (fragment)
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
15-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                        #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. #journal J. Immunol. (1989) 142:3337-3950

#ititle Diversity and diversification of HLA-A,B,C alleles. #cross-references WUID:89235215

#accession 136958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-300 ##label RES
##cross-references GB:MZ7540; NID:9187733; CDS_PID:9386890
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##cross-references GB:M24046; NID:g176816; CDS_PID:g176817
:X #length 313 #checksum 5311
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168701 ; cell surface antigen - human (fragment)
(from "PIR 50")
                                                                                                                                                                  match found in sequence:
136958 ; MHC ChlA chain - chimpanzee (fragment)
(from "PIR 50")
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#accession 168701
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46
                      qisktnaqtyreslrnlrgyynqseagshi
45 54
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37
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#authors #journal

#title

SEQUENCE

27

ACCESSIONS REFERENCE

ORGANISM

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SUMMARY

83

156034

ENTRY

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match found in sequence:
S52486; HLA-B protein alpha chain - human
(from "PIR 50")
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99 108
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99
                                                                                                                                               #cross-references MUID:92104637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IS4416; HLA-AW24 protein - human (from "PIR 50") IS4416 #type
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S52486
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SEQUENCE
Found using 'seq1' (seq1.key)
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                                                                                                                                 HLA-A9.3
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                                                                  I54493
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                                                                                                                                                                                              #authors Takiguchi, M.; Nishimura, I.; Hayashi, H.; Karakl, S.;
Kariyone, A.; Kano, K.
#journal J. Immunol. (1989) 143:1372-1378
#title The structure and expression of genes encoding serologically undetected HIA-C locus antigens.
#cross_references MUID:89309827
                                                                           156034 #type complete
gene HLA-C protein - human
#formal_name Homo saplens #common_name man
02.7u1-1996 #sequence_revision 02-7u1-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I38437 #type complete
HLA B-40011 - human
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
                                                                                                                                                                                                                                                                                                                                                               ##cross_references GB:M28171; NID:9187826; CDS_PID:9386905
X #length 366 #molecular-weight 40855 #checksum 5205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Ways, J.W.; Lawlor, D.A.; Wan, A.M.; Parham, P. #journal Immunogenetics (1987) 25:323-328 #title A Transposable Epitope of HLA-B7, B40 Molecules. #cross-references WID:87192942 #accession I38437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **status preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                 I54493 #type complete
HLA-A protein - human
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                           found in sequence: ; gene_HLA-C protein - human
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154493; HLA-A protein - human
(from "PIR 50")
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138437 ; HLA B-40011 - human
(from "PIR 50") 138437 #
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                                               56034 ; gene HLA
(from "PIR 50")
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#journal Immunogenetics (1985) 21:479-489
#title The HLA-AW24 gene: sequence, surroundings and comparison with the HLA-A2 and HLA-A3 genes.
#cross-references WUID:85206128 N'Guyen, C.; Sodoyer, R.; Trucy, J.; Strachan, T.; Jordan, B.R. Little, A.M.; Madrigal, J.A.; Parham, P. Immunogenetics (1992) 35:41-45 Molecular definition of an elusive third HLA-A9 molecule: #formal\_name Homo sapiens #common\_name man 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 07-Jun-1996 HIA-AW24 protein - human #formal\_name Homo sapiens #common\_name man 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 07-Jun-1996 S52486 #type complete
HLA-B protein alpha chain - human
#formal\_name Homo sapiens #common\_name man
08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change ##molecule\_type DNA ##residues 1.365 ##label RES ##cross-references GB.M64441; NID:9487615; CDS\_PID:9487616 XY #length 365 #molecular-weight 40831 #checksum 2547 preliminary; translated from GB/EMBL/DDBJ

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89

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##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HiA-Bl5: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Homo saptens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
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02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene name HLA-B
#length 362 #molecular-weight 40289 #checksum 9607
                                                                                                                                          #label IMM
#checksum 651
submitted to the EMBL Data Library, February 1995
S52486
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##molecule_type mRNA
##sion.c.
                                                                                                                                        #domain immunoglobulin homology #length 362 #molecular-weight 40592
                                                               ##residues 1-362 ##label HER ##cross-references EMBL:X84725
CLASSIFICATION #superfamily immunoglobulin homology
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                         ##molecule_type mRNA
##residues
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I56130
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Found using 'seq1' (seq1.key)
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162044; HLA-B*1514 - human
(from "PIR 50")
FACALA
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156130 ; HLA-B*5401 - human
(from "PIR 50")
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 #submission
                    #accession
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#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P. #journal Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P. #title HiA-Bw22: a family of molecules with identity to HiA-B7 in #cross-references MulD:92148136 #accession 172753
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Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P. J. Immunol. (1992) 148:1155-1162
HIA-BW22: a family of molecules with identity to HLA-B7 in the alpha 1-helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I72752 #type complete
HLA-B*5501 - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
122752
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XX #length 362 #molecular-weight 40496 #checksum 7953
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02-Jul-1996 #sequence_revision 02-Jul-1996
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HLA-B*5502 - human
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99 108
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#accession I72752
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172752; HLA-B*5501 - human
(from "PIR 50")
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I72753 ; HLA-B*5502 - human
(from "PIR 50")
I56130
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#title
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#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P. #journal J. Immunol. (1992) 148:1155-1162
#title HIA-Bw22: a family of molecules with identity to HLA-B7 in the alpha 1-helix.
#cross-references MUID:92148136
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#authors Hidebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P. #journal J. Immunol. (1992) 148:1155-1162
#title HiA-Bw22: a family of molecules with identity to HiA-B7 in the alpha 1-helix.
#cross-references MUID:92148136
                                                                                                                                                                                     #formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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##residues 1-362 ##label RES
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XY #length 362 #molecular-weight 40460 #checksum 7841
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HLA-B*5602 - human
                                                                                                                                                       #type complete
qiykaqaqtdreslrnlrgyynqseagsht
99 108
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99 108
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HLA-B*5601 - human
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172755; HLA-B*5602 - human
(from "PIR 50")
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172754 ; HLA-B*5601 - human
(from "PIR 50")
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ACCESSIONS REFERENCE '

SEQUENCE

83

SUMMARY

ORGANISM DATE

TITLE

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#authors Hildebrand, W.H.; Madrigal, J.A.; Belich, M.P.; Zemmour, J.; Ward, F.E.; Williams, R.C.; Parham, P. Ward, F.E.; Williams, R.C.; Parham, P. Tamunol. (1992) 149:3563-3568
#title J. Immunol. (1992) 149:3563-3568
#title Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B12 and HLA-B21 groups. Dominant #cross-references MUID:93056529
#accession 156149
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Marsh, S.G.; Willians, R.C.; Parham, P.
#journal Tissue Antigens (1992) 39:249-257
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3
#cross-references MIDD:93031775
#accession 159622
*rormal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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#formal_name Homo sapiens #common_name man
02-011-1996 #sequence_revision 02-011-1996 #text_change
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lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene name HLA-C
#length 366 #molecular-weight 40950 #checksum 5590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ###Iresidues | 1362 ##label RES | ##residues                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-366 ##label RES
##cross-references GB:M84171; NID:g187862; CDS_PID:g187863
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99 108
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99
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| IS9651 ; Lymphocyte antigen - human
| (from "PIR 50") | IS9651 #type oc
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Found using 'seq1' (seq1.key)
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I59622 ; lymphocyte antig
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                                                                                                                                                                                                                                                                                                                                                                             #authors Gussow, D.; Rein, R.S.; Meijer, I.; de Hoog, W.; Seemann, G.H.; Hochstenbach, F.M.; Ploegh, H.L.

#journal Immunogenetics (1987) 25:313-322
#title Isolation, expression, and the primary structure of HLA-Cwl and HLA-Cw2 genes: evolutionary aspects [published erratum appears in Immunogenetics 1988;27(2):158].
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Juji, T.; Kano, K.; Takiguchi, M.
#journal Immunogenetics (1993) 37:212-216
#title Molecular analysis of HLA-B39 subtypes.
#cross-references MID:93131294
#accession 154505
                                                                                                                                         #I.A.-C. heavy chain - human #formal_name man #formal_name Homo sapiens #common_name man 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 07-Jun-1996
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07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
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##residues 1-36 ##label RES
##cross-references GB:M16772; NID:g187913; CDS_PID:g386912
XY #length 366 #molecular-weight 40936 #checksum 5559
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                                                                                                                         #type complete
avv chain - human
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ymphocyte antigen - human
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99 108
               match found in sequence:
154430 ; HLA-Cwl heavy chain - human
(from "PIR 50")
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154505 ; lymphocyte antigen - human
(from "PIR 50")
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156149; lymphocyte antigen - human
(from "PIR 50")
156149 #type cc
TITLE lymphocyte antigen
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REFERENCE
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TITLE ORGANISM

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SUMMARY

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Adams, E.J.; Little, A.
Tissue Antigens (1995) 46:204-205
Identification of a novel HLA-B allele (B*4008) in a patient
with leukemia.
159655
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Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
Nature (1992) 357:326-329
                                                           #authors Arnett, K.L.; Adams, E.J.; Domena, J.D.; Parham, P. #journal Tissue Antigens (1994) 44:318-321 #title Structure of a novel subtype of B7 (B*0705) isolated from a Chinese Individual. #cross-references MUID:95184211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
02-vul-1996 #sequence_revision 02-Jul-1996 #text_change
02-vul-1996
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06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
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##cross-references GB:L41353; NID:91041064; CDS_PID:91041065
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##molecule_type DNA
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1ymphocyte antigen - human
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59655 ; lymphocyte antigen - human
(from "PIR 50")
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161903 ; lymphocyte antigen - human
(from "PIR 50")
02-Jul-1996
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#title Unusual HLA-B alleles in two tribes of Brazilian Indians. #accession 161905
PERENCE 137120
#authors Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P. #journal Nature (1992) 357:326-329
#title The The France MUD:92269955
#accession 161904
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Lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
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lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
                                                                                                                                                                           gene name HLA-B
#length 362 #molecular-weight 40362 #checksum 286
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                                                                                                               ##residues 1-362 ##label RES
##cross-references GB:M84380; NID:g187707; CDS_PID:g187708
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                                                                                preliminary; translated from GB/EMBL/DDBJ
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161904 ; lymphocyte antigen - human
(from "PIR 50")
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                                                                           ##status prel:
##molecule_type mRNA
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Page 32

qisktntqtyreslrnlrgyynqseagsht 99 108

83

SEQUENCE Found using 'seq1' (seq1.key)

GENETICS

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match found in sequence: 161906; lymphocyte antigen - human (from "PIR 50") 161906 #type oc

ACCESSIONS

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TITLE ORGANISM DATE

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##cross-references GB:M84385; NID:g187719; CDS_PID:g187720
                           gene name HLA-B
#length 362 #molecular-weight 40374
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I68850 ; lymphocyte antigen - human
(from "PIR 50")
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181231 ; lymphocyte antigen - human
(from "PIR 50")
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#authors Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Juli, T.; Kano, K.; Takiguchi, M. Juji, T.; Kano, K.; Takiguchi, M. Immunogenetics (1993) 37:212-216
#title Molecular analysis of HLA-B39 subtypes.
#cross-references MUD:93131294
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Marsh, S.G.; Willians, R.C.; Parham, P.
#journal Tissue Antigens (1992) 39:249-257
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3 #cross-references MuID:93031775
#accession 181231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte antipone applicable formal_name man formal_name Homo saplens #common_name man 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 1688-0
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1ymphocyte antigen - hunden
*formal_name Homo saplens #common_name man
02-Aug-1996 *sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
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#length 366 #molecular-weight 40784 #checksum 5046
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Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:336-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MuID:92269955
#accession 161906
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#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
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#length 362 #molecular-weight 40430 #checksum 193
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#length 362 #molecular-weight 40600 #checksum 393
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##cross-references GB:M84383; NID:9187715; CDS_PID:9187716
##molecule_type mRNA
##residues 1-362 ##*---
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##molecule_type mRNA
##residues 1-362 ##label RES
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#type complete

161907

#accession

ACCESSIONS REFERENCE

TITLE ORGANISM

1 match found in sequence: 161907 ; lymphocyte antigen - human (from "PIR 50") ENTRY

qisktntqtyreslrnlrgyynqseagshi 99 108

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SEQUENCE Found using 'seq1' (seq1.key)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors 2emmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;
Marsh, S.G.; Williams, R.C.; Parham, P.
Fisue Antigens (1992) 39:249-257
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3
alloantisera with HLA-B46 haplotypes.
#ccession 181232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181232 *type complete
1ymphocyte antigen - human
*formal_name Homo sapiens *common_name man
02-Aug-1996 *sequence_revision 02-Aug-1996 *text_change
02-Aug-1996
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| Inpubocyte antigen - human
| Inpubocyte antigen - human
| Inpupocyte antigen - human
| Inpupocyte antigen - human
| Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antigen | Inpupocyte antig
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#length 366 #molecular-weight 40772 #checksum 5003
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#length 362 #molecular-weight 40497 #checksum 885
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##cross-references GB:M84174; NID:g187868; CDS_PID:g187869
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##molecule_type mRNA
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##molearle_type mRNA
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99 108
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181232 ; lymphocyte antigen - human
(from "PIR 50") 181232 #type oc
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181233 ; lymphocyte antigen - human
(from "PIR 50")
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#cross-references MVID:93303752
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83

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#authors Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.;
Tyan, D.B.; Parham, P.
#journal Tissue Antigens (1995) 45:18-26
#title HLA-B16 antigens: sequence of the ST-16 antigen, further definition of two B38 subtypes and evidence for convergent #cross-references MUID:95242308
#accession 184488
                                                                                                                                                                                                                                                                                                                                                                                                                         Little, A.M.; Domena, J.D.; Hildebrand, W.H.; Shen, S.Y.; Barber, L.D.; Marsh, S.G.; Blas, W.B.; Parham, P. Tissue Antiqens (1994) 43:38-43 HIA-E67: a member of the HIA-E16 family that expresses the
                                                                                                                                                                                                                                                                 lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
02.Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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#formal_name Homo sapiens #common_name man
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#length 362 #molecular-weight 40376 #checksum 719
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#molecule_type Dreliminary; translated from GB/EMBL/DDBJ
##nolecule_type DNA
##residues
1-362 ##label RES
##cross-references GB:L41628; NID:g773174; CDS_PID:g773175
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##cross-references GB:L36318; NID:g793946; CDS_PID:g793947
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##residues
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#length 362 #molecul
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qifktntqtyreslrnlrgyynqseagshi
99
                                                                                                                                                        match found in sequence:
181239 ; lymphocyte antigen - human
(from "PIR 50")
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184488 ; lymphocyte antigen - human
(from "PIR 50")
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#cross-references MUID:94294981
#accession I81239
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Tissue Antigens (1995) 45:12-17
HLA class I variation in Australian aborigines:
characterization of allele B*1521.
                                                                                                                                                                                                                                                                                                             Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.; Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.; Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P. Tissue Antigens (1995) 45:177-187
The HLA-A,B.C genotype of the class I negative cell line Daudi reveals novel HLA-A and -B alleles.
                                                                                                                                                   184490 *type complete
Lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
184490
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#length 362 #molecular-weight 40354 #checksum 9646
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##residues 1-362 ##label RES
##cross-references GB:L32862; NID:g487817; CDS_PID:g487818
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159654 ; major histocompatibility complex class I - human
(from "PIR 50")
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               qicktntqtyreslrnlrgyyngseagsht
99
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99
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184490 ; lymphocyte antigen - human
(from "PIR 50")
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#authors Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.;
Geraghty, D.E.; Chaplin, D.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:1676-1680
#title Isolation and characterization of yeast artificial chromosome clones linking the HLA-B and HLA-C loci.
#cross-references WUID:91156671
                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MulD:92269955
#accession 137120
                                                                                                                                                                                                                                   MCH class I HzA-B*5104 - human
MCH class I HzA-B*5104 - human
#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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MHC cell surface entigen - human (fragment)
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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##cross-references GB:M59865; NID:g187802; CDS_PID:g187803
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##molecule_type DNA
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179640; MHC cell surface antigen - human (fragment)
(from "PIR 50")
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#length 181 #checksum 2853
                                                                                                                                                                                    match found in sequence:
137120 ; MCH class I HLA-B*5104 - human
(from "PIR 50")
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TITLE ORGANISM

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Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.;
Rickards, O.; De Stefano, G.; Watkins, D.I.
Immunogenetics (1995) 42:19-27
HIA-B alleles of the Cayapa of Ecuador: new B39 and B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Adams, B.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.;
Tyan, D.B.; Parham, P.
#journal Tissue Antigens (1995) 45:18-26
#title H.A.Bl6 antigens: sequence of the ST-16 antigen, further definition of two B38 subtypes and evidence for convergent evolution of B*3902.
#cross-references WulD:95242308
#accession I38464
                                                                                                                                                                                                                                                                                                                         138464 #type complete
MHC class I antigen - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
138464
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MHC class I antigen - human (fragment)
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
13-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene name HLA-B
#length 362 #molecular-weight 40327 #checksum 132
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##bolicule_type mRNA
##residues
##residue
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##cross-references EMBL:U14756; NID:9930328; CDS_PID:9930329
# #length 137 #checksum 5553
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; MHC class I antigen - human (fragment)
"PIR 50")
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                             qicktntqtdreslrnlrgyynqseagsht
                                                                                                                                                                                                                                  found in sequence:
; MHC class I antigen - human
"PIR 50")
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#accession I38860
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                                                                                                                                                                                                           129188 #type fragment
MHC cell surface glycoprotein - human (fragment)
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
159188
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MHC cell surface glycoprotein - human (fragment)
#formal_name Homo sapiens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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##cross-references GB:M59841; NID:g187697; CDS_PID:g187698
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##moleule_type DNA
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I79639; MHC cell surface glycoprotein - human (fragment)
(from "PIR 50")
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gene name HLA-B
#length 181 #checksum 3163
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#length 181 #checksum 2981
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qifktntqtdreslrnlrgyynqseagsht
74 83
qkykrqaqtdrvslrnlrgyynqseaahtl
74 83
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##residues 1-1
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(from "PIR 50")
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#note GENETICS

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                                                                                                                       138874 **type fragment (fragment)

#formal_name Homo sapiens #common_name man 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 138874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC class I antigen - human (fragment)
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
15-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:U15639; NID:q930332; CDS_PID:g930333
##cross-references EMBL:U15639; NID:q930332; CDS_PID:g930333
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                                                                    l match found in sequence:
138874 ; MHC class I antigen - human (fragment)
(from "PIR 50")
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138875 ; MHC class I antigen - human (fragment)
(from "PIR 50")
qifktntqtyreslrnlrgyynqseagsht
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#accession 138874
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*cross-references MUID:95317819
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##residues 1-1
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Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefano, G.; Watkins, D.I. Immunogenetics (1995) 42:19-27 HIA-B alleles of the Cayapa of Ecuador: new B39 and B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal Tissue Antigens (1994) 44:193-195
#title Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
from the sequence analysis of seven HLA homozygous cell
lines carrying HLA-C blank.
#cross-references MUID:95141286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang,
                                                                                   MHC class I antigen - human (fragment)
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
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MHC class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06.Sep-1996
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# #Length 137 #checksum 5564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-137 ##label RES
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##molecule_type mRNA
##residues 1-366 ##label RES
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138505; MHC class I histocompatibility antigen - human
(from "PIR 50")
ENTRY : 138505 #type complete
qicktntqtyreslrnlrgyynqseagsht
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99 108
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1 match found in sequence:

#authors

GENETICS

SEQUENCE

89

SUMMARY

ACCESSIONS

ORGANISM

TITLE DATE REFERENCE

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#authors Sekimata, M.; Hiraiwa, M.; Andrien, M.; Dupont, E.; Karaki,
S.; Yamamoto, J.; Kano, K.; Takiguchi, M.
J. Immunol. (1990) 144:3228-3233
#title Allodeterminants and evolution of a novel HLA-B5 CREG
antigen, HLA-B SNA.
#cross-references MUID:90217537
                                                  #type fragment
MHC class I histocompatibility antigen - human (fragment)
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156065 #type complete
MHC class I HLA-B - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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##residues 1-362 ##label RES
##cross-references GB:M33573; NID:g187745; CDS_PID:g187746
XY #length 362 #molecular-weight 40478 #checksum 9585
                                                                                                                                                                                                                                                                                                                                                                                                               . match found in sequence:
133509; MHC class I histocompatibility antigen - human (fragment)
(from "PIR 50")
ENTRY 138509 #type fragment
                                                                                                                                                                                                                                                #authors Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal Tissue Ahtigens (1994) 44:271-273
#title HLA-#5105, a newly identified B51 IEF variant.
#cross-references MUID:95176331
                                                                                                                                                                                                                                                                                                                                             ##status preliminary; translated from GB/EMBL/DDBJ#macs.tar.r.
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MHC class I HLA-Cw*0803 - human (fragment)
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137135 ; MHC class I HLA-Cw*0803 - human (fragment)
(from "PIR 50")
ENTRY
TITLE
MHC class I HLA-Cw*0803 - human (f)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene name HLA-B
#length 273 #checksum 6533
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99 108
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1156055; MHC class I HLA-B - human
(from "PIR 50")
ENTRY 150605 #type o
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                                                                                                                                                                                                                                                               #journal Tissue Antigens (1994) 44:193-195
#title Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
from the sequence analysis of seven HLA homozygous cell
lines carrying HLA-C blank.
#cross-references MUID:95141286
#accession 138507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Tissue Antigens (1994) 44:193-195
#title Identification of two new HLA-C alleles, Cw*1203 and Cw*1402, from the sequence analysis of seven HLA homozygous cell lines carrying HLA-C blank.
#cross-references mulD:95141286
#accession 138508
                                                                                                                                                                                                                      Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang,
          138507 *type complete
MHC class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 *sequence_revision 06-Sep-1996 #text_change
138507
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MHC class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
06.5ep-1996 #sequence_revision 06-Sep-1996 #text_change
06.5ep-1996
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##cross-references EMBL:U06695; NID:9469540; CDS_PID:9469541
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##cross-references EMBL:U06696; NID:9469542; CDS_PID:9469543
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##residues
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##molecule_type mRNA
##resiA...
138507; MHC class I histocompatibility antigen - human (from "PIR 50")
ENTRY #type complete
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138508; MHC class I histocompatibility antigen - human
(from "PIR 50")
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99 108
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#length 366 #mo.
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#authors

GENETICS note SEQUENCE

SUMMARY

89

ACCESSIONS

REFERENCE

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08:52:43 1997

Fri May 23

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#accession
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                                                                                                              Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P. Nature (1992) 357:326-329 Unusual HLA-B alleles in two tribes of Brazilian Indians.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
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Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
12-xmai_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
13-135
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MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo sapiens #common_name man
07.Jun-1996 #sequence_revision 07-Jun-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo saplens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
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#title Allelic variation in HLA-B and HLA-C sequences and evolution of the HLA-B alleles.
#cross-references MUID:89233295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status preliminary; translated from GB/EMBL/DDBJ#status htmolecule_type mRNA l-350 # #label RES #stoross-references GB.M28204; NLD:9576472; CDS_PID:9576473
                                                                                                                                                                                                                                           ##molecule_type mRNA
##residues 1-366 ##label RES
##cross-references EMBL:215144; NID:928356; CDS_PID:928357
XY #length 366 #checksum 5311
                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
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168748 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
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87 96
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#authors Zemmour, J.; Little, A.M.; Schendel, D.J.; Parham, P.
#journal J. Immunol. (1992) 148:1941-1948
#title The HLA-A,B " negative' mutant cell line CIR expresses a novel
HLA-B35 allele, which also has a point mutation in the
#cross-references MUID:92176661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154457
Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Welss,
E.H.
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MHC class I protein - human

#formal_name Homo sapiens #common_name man

02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

156133
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MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo sapiens *common_name man
07-Jun-1996 *sequence_revision 07-Jun-1996 *text_change
07-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title Allelic variation in HIA-B and HIA-C sequences and the evolution of the HIA-B alleles.
#cross_references WID:89233295
#accession 168750
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and evolution of the HLA-B alleles.
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##molecule_type mRNA
##residues 1-290 #label RES
##cross-references GB:M28207; NID:9576478; CDS_PID:9576479
!! #length 290 #checksum 415
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168750 ; MHC class I lymphocyte antigen - human (fragment)
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156133 ; MHC class I protein - human
(from "PIR 50")
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Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HiA-Bl5: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
                                                                                                                                                                                                                                                                                                                                                                                                                    154308 #type fragment
MHC HLA B71 - human (fragment)
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162041 #type complete
MHC HIA-B cell surface glycoprotein - human
#formal_name Homo saplens #common_name man
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
#journal Hum. Immunol. (1993) 37:192-194
#title Molecular characterization of HLA-B71 from an African American individual.
#cross-references MUID:94064392
                 ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA ##molecule_type mRNA #strossidues 1-362 ##label RES ##cross-references GB:M81798; NID:9187858; CDS_PID:9187859 ##cross-references GB:M81798; NID:9187858; CDS_PID:9187859 RY #length 362 #molecular-weight 40515 #checksum 9947
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162041; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
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##molecule_type mRNA
1-362 ##label RES
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154308; MHC HLA B71 - human (fragment)
(from "PIR 50")
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99 108
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#length 350 #cl
                                                                                                                       SEQUENCE Found using 'seq1' (seq1.key)
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156133
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#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
#fournal Tissue, M.B.; Parham, P. 209-218
#title Hill-Bis: a widespread and diverse family of HLA-B alleles.
#cross-references WulD:94367483
#accession 162042
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Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
# journal Tissue Antigens (1994) 43:209-218
# itle HLA-B1: a widespread and diverse family of HLA-B alleles.
# cross-references MUID:94367483
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                                                                                       #checksum 9515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-362 ##label RES ##cross-references GB:L11604; NID:g493162; CDS_PID:g493163
##cross-references GB:L11666; NID:g493160; CDS_PID:g493161
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                                                            gene name HLA-B
#length 362 #molecular-weight 40433
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162043 ; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
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##residues 1-362
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#authors Hildebrand, W.H.; Domena, J.D.; Parham, P.
#journal Tissue Antigens (1993) 41:190-195
#fitle Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and HLA-B51, and not a subtype of HLA-B8.
                                                                                                                                                                                                                                                                                                                                       MHC HLA-B transmembrane glycoprotein - human #formal_name Homo sapiens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1996
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                      gene name HLA-B
#length 362 #molecular-weight 40245 #checksum 9348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-362 ##label RES ##cross-references GB:M24040; NID:g187807; CDS_PID:g386898 X ##cross-references GB:M24040; NID:g187807; CDS_PID:g386898 X
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#length 362 #molecular-weight 40584 #checksum 8821
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D. Juversity and diversification of HLA-A,B,C alleles. #cross-references MUID:89235215
#accession 161859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:L07743; NID:9388314; CDS_PID:9388315
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##mseldues 1-362 ##1-c-1
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159633 ; MHC HLA-B transmembrane glycoprotein - human
(from "PIR 50")
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161859 ; MHC HLA-B14 chain - human
(from "PIR 50")
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the supertypic HLA-B
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#journal Immunogenetics (1989) 30:200-207
#title Genetic and serological heterogeneity of the supertypic HI cous specificities Bw4 and Bw6.
#cross-references MuID:89379286
#accession 154463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154463 #type fragment
MHC HLA-B38 chain - human (fragment)
#formal_name Homo sapiens #common_name man
07.Jun-1996 #sequence_revision 07.Jun-1996 #text_change
                                                                                                                                                                                                                                                                                              #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. #journal J. Immunol. (1989) 142:3337-3950

B. Immunol. (1989) 142:3337-3950

B. Diversity and diversification of HLA-A,B,C alleles. McCoss.references MUID:89235215

#accession I61860
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##rossidues 1-274 ##label RES
##erross-references GB:M29864; NID:9187675; CDS_PID:9187675
# #ength 274 #checksum 1031
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154463 ; MHC HLA-B38 chain - human (fragment)
(from "PIR 50")
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ACCESSIONS

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SUMMARY

TITLE ORGANISM DATE

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Sood, A.K.; Pan, J.; Biro, P.A.; Pereira, D.; Srivastava, R.; Reddy, V.B.; Duceman, B.W.; Weissman, S.M. Immunogenetics (1965) 22:101-121
Structure and polymorphism of class I MHC antigen mRNA [published erratum appears in Immunogenetics 1986;24
                              I54418 #type complete
MHC HLA-B7 heavy chain precursor - human
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
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MHC HLA-B8 chain - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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XY #length 361 #molecular-weight 40366 #checksum 8200
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    found in sequence:
; MHC HLA-B7 heavy chain precursor - human
"PIR 50")
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; MHC HLA-Bw41 chain - human
"PIR 50")
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#accession I54418
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; MHC HLA-B8 chain - human "PIR 50")
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                                                                                                                                                                                                                                                #authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
Weiss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title Genetics (1989) 30:200-207
#cross-references MUID:89379286
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#title Identification of the gene encoding a novel HLA-B39 subtype.
Two amino acid substitutions on the beta-sheet out of the peptide-binding floor form a novel serological epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogawa, A.; Tokunaga, K.; Nakajima, F.; Kikuchi, A.; Karaki,
S.; Kashiwase, K.; Ge, J.; Hannestad, K.; Juji, T.;
Takiguchi, M.
                                                      I68774 #type fragment
MHC HLA-B39 chain - human (fragment)
#formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I54314 #type complete
MHC HLA-B39N - human
#formal_name Homo sapiens #common_name man
02.7ul-1996 #sequence_revision 02-Jul-1996 #text_change
02.7ul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene name HLA-B
#length 362 #molecular-weight 40344 #checksum 8904
                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-274 ##label RES
##cross-references GB:M29865; NID:g187676; CDS_PID:g187677
XY #1ength 274 #checksum 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
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                     match found in sequence:
I68774 : MHC HLA-B39 chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qicktntqtdreslrnlrgyynqseagsht
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99 108
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I54314; MHC HLA-B39N - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Found using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Found using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residues 1-36
                                                                                                                                                                                                                                                                                                                                                                                    168774
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                                   (from "PIR 50")
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#authors ACCESSIONS REFERENCE

GENETICS

SEQUENCE

83

SUMMARY

ORGANISM

TITLE

7

161864 #type complete MHC HLA-Bw41 chain - human

#checksum 7954

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#accession
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#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
161864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161865 #type complete
MHC HLA-Bw42 chain - human
#formal_name Homo saplens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
161865
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MHC HIA-Bw46 - human #formal_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1996
                                                                                                                                                                                                                                                               ##residues 1-362 ##label RES ##cross-references GB:MZ4035; NID:g187820; CDS_PID:g386903 ##cross-references GB:MZ4035; NID:g187820; CDS_PID:g386903 :Y #length 362 #molecular-weight 40539 #checksum 9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:MZ4034; NID:g187822; CDS_PID:g386904
##cross-references GB:MZ4034; NID:g187822; CDS_PID:g386904
Y #length 362 #molecular-weight 40333 #checksum 8952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#accession 161865
                                                                                                             #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. #journal J. Immunol. (1989) 142:3937-3950 Diversity and diversification of HLA-A,B,C alleles #cross.references MuID:89235215 #accession 161864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
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161865 ; MHC HLA-Bw42 chain - human
(from "PIR 50")
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161863 ; MHC HLA-Bw46 - human
(from "PIR 50")
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##residues 1-3
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#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Blas, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161862 #type complete
MHC HLA-Bw65 chain - human + formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I84486 #type complete transmembrane glycoprotein - human #formal_name Homo sapiens #common_name man 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 184486
                                            ##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M24033; NID:9487818; CDS_PID:9307227
##cross-references GB:M24033; NID:9440 #checksum 9144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1362 ##label RES ##cross-references GB:M24032; NID:g187816; CDS_PID:g386902 ##cross-references GB:M24032; NID:g187816; CDS_PID:g386902 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERENCE 136956
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3337-3950
#itle Diversity and diversification of HLA-A,B,C alleles.
#cocession 161862
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##cross-references GB:L15005; NID:g493154; CDS_PID:g493155
                          preliminary; translated from GB/EMBL/DDBJ
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##molecule_type mRNA
##molecule_type mRNA
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184486 ; transmembrane glycoprotein - human
(from "PIR 50")
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99 108
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161862; MHC HLA-Bw65 chain - human
(from "PIR 50") 161862 #type oc
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Found using 'seq1' (seq1.key)
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##residues 1-3
I61863
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                          ##status
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##residues
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(from "PIR
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#journal J. Exp. Med. (1988) 168:2319-2335
#title Three spontaneous H-2D-b mutants are generated by genetic micro-recombination (gene conversion) events: Impact on the H-2-restricted immune responsiveness.
#cross-references MUID:89067835
#accession 155665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemmi, S.; Geliebter, J.; Zeff, R.A.; Melvold, R.W.;
Nathenson, S.G.
J. Exp. Med. (1988) 168:2319-2335
Three spontaneous H-2D-b mutants are generated by genetic micro-recombination (gene conversion) events: Impact on the
                                                                                                                                                                                                                                                                                      155665 #type fragment
H-2D cell surface glycoprotein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170693 #type fragment
H-2D cell surface glycoptoctin - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
02-Aug-1996_#sequence_revision 02-Aug-1996 #text_change
#length 362 #molecular-weight 40378 #checksum 9463
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemmi, S.; Geliebter, J.; Zeff, R.A.; Melvold, R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-337 ##label RES
##cross-references GB:M37680; NID:g293733; CDS_PID:g293734
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##molecule_type mRNA ##rasiance
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##molecule_type mRNA
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170693 ; H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
                                                                                                                                                                                                                                                . match found in sequence:
155665; H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
ENTRY 155665 #type fragment
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gene name H-2D
#length 337 #checksum 9859
                                                                                                                              qisktntqtyrenlrialryynqseagshi
99
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#authors Schepart, B.S.; Takahashi, H.; Cozad, K.M.; Murray, R.;
Ozato, K.; Appella, B.; Frelinger, J.A.
#journal J. Immunol. (1986) 136:3489-3495
#title The nucleotide sequence and comparative analysis of the H2D-P class I H-2 gene.
#cross-references wIUD:86169714
#accession 155961
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Nucleotide sequence analysis of H-2D(f) and the spontaneous in vivo H-2D(fm2) mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155961 #type complete
MHC class I H2D-P protein - mouse
#formal_name Mus musculus #common_name house mouse
26-7u1-1996 #sequence_revision 26-7u1-1996 #text_change
26-Ju1-1996
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MHC class I-alpha - mouse
#formal_name Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 359/1
#length 368 #molecular-weight 41342 #checksum 7387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-368 ##label RES
##cross-references GB:Ml2381; NID:9199418; CDS_PID:9387454
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##cross-references GB:M86502; NID:g199306; CDS_PID:g199307
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90/1; 182/1; 274/1; 313/1; 324/1; 337/1
                             gene name H-2D
#length 337 #checksum 9564
                                                                                                                                                                                                                                                                                                                                                                                                                     found in sequence:
; MHC class I H2D-P protein - mouse
"PIR 50")
                                                                                                                                                                                                                                            qkakgqeqwfrvslrnllgyynqsaggsht
74 83
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; MHC class I-alpha - mouse
"PIR 50")
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#accession 157814
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#journal Immunogenetics (1991) 34:62-65
#title Manufacture of a functional cDNA for the H-2Db molecule using a retroviral shuttle vector.
#cross-references MUID:91310091
#accession 148323
                                                                                                                                                                                                                                                                                                                                                                                                       Watts, S.; Vogel, J.M.; Harriman, W.D.; Itoh, T.; Stauss, H.J.; Goodenow, R.S.
J. Immunol. (1987) 139:3878-3885
DNA sequence analysis of the C3H H-2KK and H-2DK loci.
Evolutionary relationships to H-2 genes from four other
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MHC class I protein - rat (fragment)
#formal_name Rattus norvegicus #common_name Norway rat
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
154531
                                                                                                                                                                                                                                                                                                         MHC H-2D-b protein - mouse
#formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
               #molecular-weight 41084 #checksum 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 362/1
gene name D(b) gene
#length 362 #molecular-weight 40836 #checksum 8991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
##cross-references EMBL:X52490; NID:950671; CDS_PID:950672
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154531 ; MHC class I protein - rat (fragment)
(from "PIR 50")
                                                                                                                                                                                                                                                                                         I56002 #type complete
MHC H-2D-b protein - mouse
                                                                                                                                 qkakgqeqwfrvnlrillgyynqsaggsht
99
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99 108
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156002 ; MHC H-2D-b protein - mouse
(from "PIR 50")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #cross-references MUID:88060499
#accession I56002
gene name H-2Df
#length 365 #mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse strains
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156002
                                               Found using 'seq1' (seq1.key)
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Salgar, S.K.; Kunz, H.W.; Gill, T.J.
Immunogenefics (1995) 42:244-233
Nucleotide sequence and structural analysis of the rat RT1.Eu
and RT1.Aw31 genes, and of genes related to RT1.0 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mauxion, F.; Sobczak, J.; Kress, M.
Immunogenetics (1989) 29:397-401
Characterization of five distinct cDNA clones encoding for
class I RTI antigens.
#authors Salgar, S.K.; Sawal, H.; Kunz, H.W.; Gill, T.J.
# fjournal immunogenetics (1994) 39:447
# title Cloning and expression of the rat class I MHC gene RT1.Al.
# cross-references MUID:94245290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154554 *type complete
MHC class I RTI.Aw3 protein - rat
*formal_name Nattus norvegicus *common_name Norway rat
02-Aug-1996 *sequence_revision 02-Aug-1996 *text_change
02-Aug-1996
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MHC RT16 protein - rat (fragment)
#formal_name Rattus norvegicus #common_name Norway rat
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residues 1-370 ##label RES
##cross-references GB.L26224; NID:g710562; CDS_PID:g710563
RY #length 370 #checksum 6182
                                                                                                                                preliminary; translated from GB/EMBL/DDBJ
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##molecule_type mRNA
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154554; MHC class I RT1.Aw3 protein - rat
(from "PIR 50")
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168771; MHC RT16 protein - rat (fragment)
(from "PIR 50")
168771, #type fragment
                                                                                                                                                                                                                                                                                                                                                                                                                           qkakgneqnyrvslrnlrgyynqseggsht
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89 98
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##residues
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                      88
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Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal Nature (1988) 335:268-271
#title HiA-A and Dolymorphisms predate the divergence of humans and chimpanzees #cross-references MUID:88319000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergmans, A.M.C.; Tijssen, H.; Lardy, N.; Reekers, P. Hum. Immunol. (1993) 38:159-162
Complete nucleotide sequence of HLA-B*0703, a B7 variant (BPOT).
S60601
                                                                                                                                                                                                                                                                                                                                                                              S07113 #type complete
class I histocompatibility antigen Ch39 alpha chain -
champanzee
#formal_name Pan troglodytes #common_name chimpanzee
01-Dec-1993 #sequence_revision 01-Dec-1993 #text_change
S07113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soubol #type complete
HLA-BPOT (class!) protein - human
#formal_name Homo sapiens #common_name man
20-Jul-1996 #sequence_revision 20-Jul-1996 #text_change
20-Jul-1996
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##residues 1-362 ##label BER
##cross-references EMBL:X64454
X #length 362 #molecular-weight 40529 #checksum 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
1-363 ##label LAW
#length 363 #molecular-weight 40540 #checksum 610
##molecule_type mRNA
##residues 1-296 ##label RES
##cross-references GB:M24023; NID:g205448; CDS_PID:g205449
XX #length 296 #checksum 9381
                                                                                                                                                                                                                                                                                                                      match found in sequence:
S07113 ; class I histocompatibility antigen Ch39 alpha chain
(from 'PIR 50")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50601 ; HLA-BPOT (class1) protein - human
from "PIR 50")
                                                                                                                                                                                                    qkakgneqnyrvslrnlrgyynqseggsht
25 34
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99 108
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S60601; HLA-BPOT (classI
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#journal
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1 match found in sequence:
1A02_PANTR; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSO (from "Swiss-Prot 34")
1D 1A02_PANTR STANDARD; PRT; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                   #authors Murray, R.; Pederson, K.; Prosser, H.; Muller, D.; Hutchison III, C.A.; Frelinger, J.A.
#journal Nucleic Ace, (1988) 16:9761-9773
#title Random oligonucleotide mutagenesis: application to a large protein coding sequence of a major histocompatibility complex class I gene, H-2DP.
#cross-references MUID:89041564
#accession S03687
                                                                                                                                                S03687 #type fragment
Class I histocompatibility antigen H-2DP alpha chain - Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N [1]

X ENDLINE; 90201944.

A LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;

LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;

LIMUNOL. REV. 113:147-185(1990).

-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-RASP) PO3989; 1183.

R EMBL; M30679; G176825; -.

R PROSITE; PS00299; IG_MHC.

R PROSITE; PS00299; IG_MHC.

MMC I: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
A-5 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                              (fragment)
#formal_name Mus musculus #common_name house mouse
21.Nov-1993 #sequence_revision 21-Nov-1993 #text_change
503687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CHIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
PAN TROGLODYTES (CHIMPANZEE).
EUKARYOTA: METAGOA: CHONDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
                                                                                CONNECTING PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                   preliminary
1-90 ##label MUR
#length 90 #checksum 1722
qiyktntqtdreslrnlrgyynqseagsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qnakdheqsfrvslrnllgyynqskg
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Found using 'seq1' (seq1.key)
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362
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TRANSMEM
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gkvkahsqtdrenlrialryynqseagsht
       PO5534; P30448; P30449;
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DISULFID
VARIANT
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VARIANT
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SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
     83
                                                                                                                                                                                                                                                          . match found in sequence:
1A23_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
(from 'Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . match found in sequence:
1A24_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A24_HUMAN STANDARD; PRT; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHALIN A-23(A9).
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*2301).
MEDELINE; 92104637.
LITLE A.-M., MADRIGAL J.A., PARHAM P.;
IMMUNOGENETICS 35:41-45(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE IMMUNE SYSTEM.
--- SUBBUILT: INDER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
--- POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HALA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 97E6CE8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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B1C21094 CRC32;
                                                                                                                                                                                                                                                                                                                   365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gkvkahsqtdrenlrialryyngseagsht
99
                                                                                                                                                        qisktnaqtyreslrnlrgyynqseagshi
125 188 BY 227 283 BY 110 110 BY 362 AA; 40487 MW; 41' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
MM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M64742; G187618; -. HSSP; P01892; 1HHG. MIM; 142800; -. PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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1115
2207
2299
3309
333
1110
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DISULFID 12
DISULFID 22
CARBOHYD 13
SEQUENCE 365
d using 'seq1'
                                                                                                                                                                                                                                                                                                                1A23_HUMAN
P30447;
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TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
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SIGNAL
CHAIN
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN A-24(A9).
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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-!- FOLX MORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401, A*2401 A A*2401, A*2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-206 FROM N.A.

SEQUENCE OF 26-206 FROM N.A.

GAO X., MCCLUSKEY J.;

SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REF.
01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN
PRECURSOR (AW-24).
                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
G -> A (IN A*2402 AND A*2403).
C -> W (IN REF. 5).
DG -> EW (IN A*2402).
A -> T (IN A*2402, A*2403 AND RE W).
DE23D06E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (A*2401).
MDELINE; 85206128.
N'GYEN C., SODYER R., TRUCY J., STRACHAN T., JORDAN B.R.;
IMMONOGENETICS 21:479-489(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J., WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.; NATURE 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN; SIGNAL; POLYMORPHISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (XXX-1988) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNECTING PEPTIDE
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MEDLINE; 9210463).
LITTLE A.-M., MADRIGAL J.A., PARHAM
IMMUNGENETICS 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E 365 AA; 40644 MW; 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (A*2402).
MEDLINE; 92269955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E; PS00290; IG_MHC
TRANSMEMBRANE; GL
                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS (A*2401).
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2006
2006
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MICROGLOBULIN).
-!- POLYMORPHISM: THE ONLY ALLELE OF A-32 KNOWN IS A*3201 WHICH
                                                                                             SEQUENCE OF 25-298 FROM N.A. (A*3201).
MEDLINE; 87058961.
WAN A.M., ENNIS P., PARHAM P., HOLMES N.;
J. IMMUNOL. 137:3671-3674(1986).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                        SUBMITTED (DEC-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rnvkahsqtdreslrialryyngseagsht 99 108
  [1]
SEQUENCE FROM N.A. (A*3201).
                                                                                                                                                                                                                                                                                     SHOWN HERE.
EMBL, U03907; G432996; -.
PIR, A26088; HLHU32.
HSSP; P01892; 1HHG.
MIM, 142800;
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sed1,
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 MHC I;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using
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FT WE BEAR OF COURT OF THE STATE OF THE STAT
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1A32_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
(from "Swiss-Prot 34")......
                                                                           match found in sequence:
1A222-HUMAN; H.A. CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A25_HUMAN STANDARD; PRT; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN A-25(A-10).
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS SHOWN HERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A32_HUMAN STANDARD; PRT; 365 AA.
P10314.
01-MAR-1995 (REL. 10, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                           01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131A8F20 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN; SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (A*2501). MEDLINE; 90207291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M32321; G307225; --. PIR; A35997; A35997. HSSP, P01891; 1145B. MIM; 142800; -. PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 AA; 4121
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC I; TRANSMEMBRANE;
SIGNAL 1 2
CHAIN 25 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROGLOBULIN).
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TRANSMEM
DOMAIN
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DISULFID
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                                                                                                                                                              P18462
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

GLYCOPROTEIN; SIGNAL.

ALPHA CHAIN A-32(AW-19). EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE

CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 71FA71A9 CRC32;

41048 MW;

5 AA; 4104 (seq1.key)

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. match found in sequence:
1B01_GONGO; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")

ID 1B01_GONGO STANDARD; PRT; 362 AA.

AC P30379;
                                                                                                                                                           01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA GORILLA (LOWIAND GORILLA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
J. EXP. MED. 174:1491-1509(1991).
-I- EUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYCOPROTEIN; SIGNAL.
4 BY SIMILARITY.
2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60255; G22866; --
PIK; JH0539; JH0539.
HSSP; P03399; JH0539.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYC
SIGNAL
1 25
CHAIN
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rnmkasaqtdrenlrialryynqseagsht 95

Fri May 23 08:52:43 1997

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1 match found in sequence:

1B01_PANTR : CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSO (from "Swiss-Prot 34")

1D 1B01_PANTR STANDARD;

AC P13750.

DT 01-JAN-1990 (REL. 13, CREATED)

DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR

DE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (FEB-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; X13115; G755776; -.
EMBL; X13115; G755776; -.
PROSTE; P03899; 115A.
PROSTE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLXCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                           PAN TROGLÓDYTES (CHIMPANZEE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
U
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER
KKLEIN J.;
EMBO J. 7:2765-2774(1988).
GOGO-B0101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 2E33E2B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
5395FFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21

111 2

111 2

DOMAIN 203 294

DOMAIN 295 305

306 329

VALIN 330 359

TEID 121 184 E

TD 223 279 E

TD 223 279 E

359 AA; 40173 MW; 55

41' (seq1.key)
                                                                                                                                                                       qtskaqaqtdrenlrialryynqseagsht
qq 108
                                                                                                             2 AA; 40170 MW;
(seq1.key)
                                                                                                                                                                    [-----|
          25
115
207
209
309
333
125
227
227
110
                                                                                                                          using 'seql'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
REVISIONS.
                      DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAYER W.;
                                                                                     DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC I; TH
NON_TER
SIGNAL
CHAIN
           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
89
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1 match found in sequence:
1B02_GORGO; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B-7 B*0702 ALPHA CHAIN
                                                                                                                                                                                          MEDILINE; 92078860.

MEDILINE; 92078860.

L. LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;

L. SER. MED. 174:1491-1509(1991).

-!- FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMURE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; X60693, 262868; -.

RASEP; P03989; 1HSA.

R PROSITE; P800290; IG_MC.

MICL I, TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

SIGNAL

TARGELOBULIN.

R PROSITE; P800290; IG_MC.
                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CLASS I HISTOCOMPATIBILITY ANNOTATION GOGO-B0102 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOIJO2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
01-FFB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
PRECURSOR (B7.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARXOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 match found in sequence:
1802_HUMAN ; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
(from "Swiss-Prot 34")
(from "Swiss-Prot 34")
AC PO1889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                             362 AA
                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qtskaqaqtdrenlrialryynqseagsht
99 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 362 AA; 40204 MW; using 'seq1' (seq1.key)
                                            STANDARD;
                                                                                                                                                                  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 90207291.
                                          1B02_GORGO
P30380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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DOMAIN
DOMAIN
                                             89
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[2]
REVISIONS.
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CARBOHYD
SEQUENCE
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TRANSMEM
DOMAIN
DISULFID
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DOMAIN
DOMAIN
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  POPE STATE OF STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 match found in sequence:
1B02_PANTR; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSO
(from "Swiss-Prot 34")
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDDIINE: 85287366.
SOOD A.K., PEND P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
DUCEMAN B.W., WEISSMAN S.M.;
IMMUNOGENETICS 22:101-121(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-7 B*0702.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 80088278.

ORR H.T., LOPEZ DE CASIRO J.A., LANCET D., SIROMINGER J.L.;
BIOCHEMISTRY 18:5711-5720(1979).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                              PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D., KRENGY A.M., LIAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T., SALTER R.D., ZEMMONG J.; COLD SPRING HARB. SYMP. QUANT. BIOL. 54:529-543(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE IMMUNE SYSTEM.
-:- SUBMIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; M32117, G337221, -.

EMBL; M16102; G307217; ALT_SEQ.

EMBL; M20905; G1213467; -.

PIR; B35997; B35997.

PIR; B35997; B35997.

MMM: 142830; -.

PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALA -> GPW (IN REF. 3).

Q -> E (IN REF. 5).

W -> S (IN REF. 3).

R -> G (IN REF. 3).

GL -> RP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1802_PANTR STANDARD; PRT; 362 AA P13751; 01-JAN-1990 (REL. 13, CREATED) 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
266 266
268 268 R
297 297 8
314 315
ACE 362 AA; 40460 MW; F
19 'seql' (seql.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qiykaqaqtd'eslrnlrgyynqseagsht
99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                 25-295
                                                       SEQUENCE FROM N.A. MEDLINE; 90315860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
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DISULFID
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CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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128E
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1 match found in sequence:
1B03_GORGO ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")

ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-ARR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CLASS I HISTOCOMPATIBILITY ANNIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA (LOWLAND GORILLA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
BURAN TROGLODYTES (CHIMPANZEE).
EUKRANOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                      MAYER W.;
SUBMITTED (FEB-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTICENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; X13116; G38209; -.
PIR; S03538; S03538.
HSSP; P03889; 1HSA.
PROSITE; PS00299; 1HSA.
MRC I; TRANSMERNE; GIXCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

BEDLINE, 92078660.

LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;

J. EXP. MED. 174:1491-1509(1991).

-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMONE SYSTEM.
-! SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                               .
U
                                                                                                                                                         MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER KLEIN J.;
EMBO J. 7:2765-2774(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4BF65A6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qisktnaqtyreslrnlrgyynqseagshi
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IN 207
IN 299 3:
FM 309 3:
333 36.
) 125 188
227 283
120 110
120 110
1 10 110
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PIR; JH0541; JH0541.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC.
                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE; 89030641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; PRIMATES
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GLYCOPROTEIN; SIGNAL.

MHC I; TRANSMEMBRANE; SIGNAL 1 2

83

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qicktntqtdreslrnlrgyynqseagsht
99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                         match found in sequence:
1B04_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQUENCE FROM N.A.
AX MEDLINE; 892323215.
RA PARHAM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
C. -- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO C.THE IMMUNE SYSTEM.
CC --- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-CC MICROGLOBULIN).
DR HCROGLOBULIN).
DR HSSP; P03989; 1HSA.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
MIM: 142830:
DR PROSITE; PS00290; IG_MHC.
MIM: 178ANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
MIM: 178ANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

HANDER OF ANTIGEN ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-8 B*0801.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                        BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GCGO-BOLO3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FEA6A941 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
1467BEB CRC32;
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                                                                               25

115 206

207 298

299 308 CON...

IN 333 362 CYTOP

SULFID 125 188 BY CYTOP

SEQUENCE 362 AA; 40248 MW;

and using 'seql' (seql.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qtskaqaqtdrenlrialryynqseagsht
99 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using 'seql' (seql.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (from "Swiss-Prot 34")
D 1B04_HUMAN STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30460;
                                                   CHAIN
FTT C C C FTT D D FTT
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1 match found in sequence:
1B07_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B07_HUMAN STANDARD, PRT; 362 AA.
AC P30462;
                                                                                                                                                                                                                                                                                                                                       MEDILINE; 89235215.

MEDILINE; 89235215.

D. J. IAMUON L. 142:3937-3950(1989).

- 1. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

- 1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; MA1040; 6386898; -...

EMBL; MA2040; 6386898; -...

EMBL; MA2040; 14SA.

MIN; 142830; -...

PROSENTE; PROSENTE; DAMC.

MAC I; TRANSMEMBRANE; GLAMC.

TIGHAL

1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-14 B*1401.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                              01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 9BED8199 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE 362 AA; 4035 using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1114
206
208
309
333
362
1110
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
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BW-65(B-14) B\*1402 ALPHA 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B\*1402 ALPHA CHAIN
PRECURSOR. HLAB. HOMO SAPIENS (HUMAN) EUKARYOTR; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA; EUTHERIA; PRIMATES. 1 match found in sequence:
1B08\_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
(from "Swiss-Prot 34")
1D 1B08\_HUMAN STANDARD; PRT; 362 AA.
AC P30463;

SEQUENCE FROM N.A. MEDLINE; 89235215.

qifktntqtdreslrnlrgyynqseagsht 99

89

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23 08:52:43 1997

Fri May

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DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
        FT DI
FT DI
SQ SI
Found
                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match found in sequence:
1B10_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA
(from "Swiss-Prot 34")
1D 1B10_HUMAN STANDARD; PRT; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-65(B-14) B*1402.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN BW-75(B-15) B*1502.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
J. IMMUNDL. 142.3937-3950(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICKOCHOBULIN).
EMBL; M24032; G386902; --
HSSP; P03989; 1HSA.
MIM: 142890; --
MIM: 142890; --
MIM: 12800; --
MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE; 92196792.
LITLE A.-M., PARHAM P.;
TISSUE ANTIGENS 38:186-190(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM.

-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; W75138; G137710; -.

HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; BE68AC9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qicktntqtdreslrnlrgyynqseagsht
                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                              2 AA; 40342
(seq1.key)
                                                                                                                                                                                                                                 1114
206
206
309
333
362
1110
188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1114
206
208
309
333
110
                                                                                                                                                                                                                             255
115
207
310
310
1105
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRECURSOR.
                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC I;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                using
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
     83
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match found in sequence:
1811_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
(from "Swiss-Prot 34")

1D 1811_HUMAN STANDARD; PRT; 362 AA.
AC P30465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 match found in sequence:
1812-HUMAN; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
(from "wiss-Prot 34")
ID 1812_HUMAN STANDARD; PRT; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN BW-72(BW-70) B*1503.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE; 93056508

MEDILINE; 93056508

MEDILINE; 93056508

MEDILINE; 93056508

MARTICAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,

LITTLE A.W., DT TOT E.D., PARHAM P.;

J. IMMUNOL, 149:3411-3415(1992)

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; X61709; G32189; -.
PIR: S16789; S16789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR ALPHA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;, 99D770546 CRC32;
BY SIMILARITY.
BY SIMILARITY.
8CF9BCD0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                              qisktntqtyreslrnlrgyynqseagshi 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qisktntqtyreslrnlrgyynqseagsht
JISULFID 125 188 B'
DISULFID 227 227 B'
DISULENCE 362 AA; 40338 MW;
using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P03989, 1HSA.
MIM, 142830; -.
PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 362 AA; 4038 using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC I; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN)
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EMBL, X03664, G871296, -.
EMBL, X03664, G871296, JOINED.
EMBL, L38504, G895271; -.
PIR, B25929, HLHUBK.
HSRP, P03989, 1HSA.
MIM, 142830; -.
MIM, 142830; -.
MRC I; TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL.
SIGNAL 1
24
CHAIN 25 362 HLA CLASS I HISTC
                                                                                                                                                                           sed1,
                                                                                          DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                             DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                         using
                                                       SIGNAL
                                                                                 DOMAIN
                                                                 CHAIN
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                         l match found in sequence:

lB13_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN

(from "Swiss-Prot 34")

lD 1813_HUMAN

AC P30466;

DT 01-APR-1993 (REL. 25, CREATED)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN

BE PRECURSOR.

GN HLAB.

OC EUTHERIA: PRIMATES.

C EUTHERIA: PRIMATES.

RN H13

SEQUENCE FROM N.A.

RN MEDLINE; 89235215.

RA PARHAM P., LAMIOR D.A., LOMEN C.E., ENNIS P.D.;

RA PARHAM P., LAMIOR D.A., LOMEN C.E., ENNIS P.D.;

C -1 FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

C THE IMMUNE SYSTEM.

C -1 SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-62 B*1504.
EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                              5
F
       01-APR-1993 (REL. 25, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
PRECURSOR.
                                                      HLAB.
HOMO SAPIENS (HUMAN).
EUTAERIA: PETRAPODA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E80FC24C CRC32;
                                                                                                                                                                                                                                       GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                            qisktntqtyreslrnlrgyynqseagsht
99 108
                                                                                                                                                                                                                                                                                                                                                         AA; 40406 MW; (seq1.key)
                                                                                                                                                                                                                                       MHC I; TRANSMEMBRANE
                                                                                                                                                                                                                                                                         25
1115
2207
2299
3310
334
1110
                                                                                                                                                                                                                                                  1
22
                                                                                                                                                                                                                                                                                                                                                                   sed1,
                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                   using
                                                                                                                                                                                                                                                                          DOMAIN
83
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match found in sequence:
1B15_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN (from "Swiss-Prot 34")
ID 1B15_HUMAN STANDARD; PRT; 362 AA.
                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-18 B*1801.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-PAR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECURSOR (B-27K) (B27.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 86-107 AND 171-181.
MEDLINE; 86042671.
VEGA M.A., EZGUERRA A., ROJO S., APARICIO P., BRAGADO R.,
LOPEZ DE CASTRO J.A.;
PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-!- SUBUNTY: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PARHAM P., ARNETT K.L., ADAMS E.J.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
BEDLINE; 86220133.
SERAANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 038EC3FC CRC32;
                                                                                             PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gisktntgtyreslrnlrgyyngseagsht
99 108
                                                                                                                                                                                                                                                                                                                                                                                                                                  MΜ.
                                                                                                                                                                                                                                                                                                                                                                                                                               (seq1.key)
MICROGLOBULIN).
EMBL; M24039; G386899;
HSSP; P03989; 1HSA.
MIM; 142830; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------
                                                                                                                                                                                                                 25
115
2007
210
310
334
110
125
227
362 AA;
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

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match found in sequence:
1821_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN (from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 89339610.
OOBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
OOBAT., HAYASHI H., FARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
IMMUNOSENETICS 30:76-80(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBMUNIT: DIERR OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                     01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA CHAIN B-35 B*3501.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
 ALPHA CHAIN B-27 B*2702.
            EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                              CONNECTING PEPTIDE
                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 9798FOBB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NY SIMILARITY.
NY SIMILARITY.
NY SIMILARITY.
AECIC675 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                  362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                            |-----|
qickakaqtdrenlrialryyngseagsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M28115; G189673; --
EMBL; M28109; G187673; --
EMBL; M28110; G187673; JOINED.
EMBL; M28111; G187673; JOINED.
EMBL; M28112; G187673; JOINED.
EMBL; M28113; G187673; JOINED.
EMBL; M28113; G187673; JOINED.
PIR; A45860; A45880.
                                                                                                                    MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40455 MW;
      25

IN 209

IN 299

TEM 309

33 36,

110 110

125 188

227 AA, 40397

1 (seq1.key)
                                                                                                                  40397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE 362 AA; 4045
'Seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC I; TRANSMEMBRANE;
SIGNAL 1
                                                                                                                                                                                                                                                                                               1B21_HUMAN
           DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                             using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
89
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ان
                                                                                 match found in sequence:
1822 HUMAN ; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . match found in sequence:

1B23_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN

(from "Swiss-Prot 34")

AD 1B23_HUMAN STANDARD; PRT; 362 AA.

AC P30469;

DT 01-APR-1993 (REL. 25, CREATED)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN

DE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-35 B*3502.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                          MEDLINE; 91365651.
CHERTROFF L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
HUM. IMMUNOL. 31.153-158(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                     01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; D7B5C2C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                              362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN; SIGNAL.
qifktntqtyreslrnlrgyynqseagshi
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qifktntqtyreslrnlrgyynqseagshi
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40564
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M63454; G403145; -. HSSP; P03989; 1HSA. MIM; 142830; -. PROSITE; PS00290; IG_MHC.
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CE 362 AA; 4056
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC I; TRANSMEMBRANE;
SIGNAL 1
                                                                                                                           1B22_HUMAN
P30468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLAB.
                                                                                                                             OSSIGNATION
    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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Fri May 23 08:52:43 1997

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83
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1B4_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN (from "Swiss-Prot 34")
1D 1B24_HUMAN STANDARD; PRT; 354 AA.
AC P30470;
                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-35 B*3503.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-35 B*3504.
                        SEQUENCE FROM N.A.
MEDLINE; 92176661.
ZEMMOUR J., LITTLE A.M., SCHENDEL D.J., PARHAM P.;
J. LITTLE A.M., SCHENDEL D.J., PARHAM P.;
J. IMMOND. 148:1941-1948(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL, MB1798; G187859; -.
HSSP; PO3939; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MADLINE, 2226995A

WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
LEVING G.M., HUGHES A.L., LETVIN N.L.;
NATURE 357:329-333(1992)

-I. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.

-I. SUBDINIT: DIABLER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
4222D30A CRC32;
                                                                                                                                                                                             GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M86403; -; NOT_ANNOTATED_CDS.
HSSP; P03989; 1HSA.
MIM; 142830; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                qifktntqtyreslrnlrgyynqseagshi
99
                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                              40515
                                                                                                                                                                                                                                                                                                                                                                                62 AA; 4051
' (seq1.key)
                                                                                                                                                                                               TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN)
 EUTHERIA; PRIMATES
                                                                                                                                                                                                               25
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                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                             MHC I;
SIGNAL
                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                         CHAIN
83
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1 match found in sequence:
1B25_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
(from "wiss-Prot 34")
ID 1B25_HUMAN STANDARD; PRT; 362 AA.
AC P30471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-35 B*5505.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 92269955.
BELICH M.P., MADIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
NATURE 357:326-329(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                           01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
PRECURSOR (B35-G).
                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 6564795A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

1; B404A7FA CRC32;
                                                         CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M84385; G187720; -.
HSSP; P03899; 1HSA.
MIM; 142880; -.
PRESITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                        qifktntqtyreslrnlrgyynqseagshi
91 100
                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM;
                                                                                                     4 AA; 39617
(seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REQUENCE 362 AA; 4037 using 'seq1' (seq1.key)
 106
108
300
324
354
102
180
275
                                                                                                                                                               1-----
                                                                                                     354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
1115
207
209
309
333
1110
125
227
                                                                                                                 nsing 'seq1'
                                 DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                        SOLUTION
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qifktntqtyreslrnlrgyynqseagsht 99 S

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1B28_HUMAN
P30474;
                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                  DISULFID
DISULFID
SEQUENCE
                                                                                                                 DOMAIN
                                                                                                                            DOMAIN
                                                                                                                                                                                                                 using
                                                                                              CHAIN
match found in sequence:
B36 HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3506 ALPHA CHAIN (from "Swiss-Prot 34")

(from "Swiss-Prot 34")

D 1826 HUMAN STANDARD;

O 70472-1993 (REL. 25, CREATED)

O 1-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

O 1-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3506 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B*3507 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-35 B*3506.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                    -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA CHAIN
                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
MEDLINE; 93303752.
THEILER G., PANDO M., DELFINO J.M., TAKIGUCHI M., SATZ M.L.;
TISSUE ANTIGENS 41:143-147(1993).
                                                                                                                                                                                                                       -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL: M84381; 613712; -.
HSSP; P03989; 1HSA.
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 92269955.
BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
NATURE 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN),
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B*3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 match found in sequence:
1B27_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
(from "Swiss-Prot 34")
ID 1B27_HUMAN STANDARD; PRT; 362 AA.
AC P30473;
                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                             Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

575079D9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 1
                                                                                                                                                                                                                                                                                 GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qifktntqtyreslrnlrgyynqseagshi
99 108
                                                                                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                           40514
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 362 AA; 4051 using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                      PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                               MHC I; TRANSMEMBRANE; CSIGNAL 1 24 CHAIN 25 362
                                                                                                                                                                                                                                               HSSP; PUL-
TM: 142830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                        DOMAIN
        1 match
                                    89
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HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-35 B*3507.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
   ဥ
-! - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
               THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 9F979909 CRC32;
                                                                                                                                  GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                       Ψ.
                                           MCROGLOBULIN).
EMBL; L04695; G187893; -.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                  40497
                                                                                                                                                                                                N 115 114

N 207 298

N 209 308

NEM 309 332

N 333 362

N 110 110

110 110

110 125 188

FID 125 188

FID 227 AA; 40497

3 'seq1' (seq1.key)
                                                                                                                                  MHC I; TRANSMEMBRANE;
SIGNAL 1 2
```

qifktntqtyreslrnlrgyynqseagshi 99 108

1 match found in sequence:
1828\_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B\*3508 ALPHA CHAIN
(from "Swiss-Prot 34")
DDW: 362 AA. SEQUENCE FROM N.A.
MEDLINE; 94186367.
STEINLE A., REINHARDT C., NOESSNER E., UCHANSKA-ZIEGLER B.,
ZIEGLER A., SCHENDEL D.J.;
HUM. IMMUNOL. 38:261-269(1993).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B\*3508 ALPHA CHAIN
PRECURSOR. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. M. L.; THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN). SATZ THEILER G., PANDO M., DELFINO J.M., TAKIGUCHI M., TISSUE ANTIGENS 41:143-147(1993). GLYCOPROTEIN; SIGNAL. EMBL; L04696; G184216; EMBL; L04696; G184216; EMBL; S22551; G297143; PIR; S32754; S32755.
HSSP; P03989; 118A.
MIM; 142830; PROSITE; PS00290; IG\_MHC.
MHC I; TRANSMEMBRANE; GLYCO
SIGNAL
CHAIN
25 362 [1] SEQUENCE FROM N.A. MEDLINE; 93303752.

HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-35 B\*3508.

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PACOOPER PRESE - 1 TTAPA MONTH PROPER PROPERTY P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 match found in sequence:
1B31_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N SEQUENCE FROM N.A.

X MEDLINE; 93131294.

X KATO N., KARAKI S., KASHIWASE K., MUELLER C., AKAZA T., JUJI T.,

A KATO N., TARIGUCHI M.

L IMMUNGENETICS 37:212-216(1993).

-! FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMARR OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).

C MICROGLOBULIN).

EMBL; M94051; G184164; -.

R EMBL; M94051; G184168; -.

R ESSP; P03989; 1HSA.

MIM: 142830; -.

R PROSITE; PS00290; IG_MMC.

MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-39 B*3901.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
PRECURSOR (B39.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLAB.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
        EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                              IX SIMILARITY.
IX SIMILARITY.
IX SIMILARITY.
E067BD80 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FIDE607E CRC32;
                                                                                                                                                    CYTOPLASMIC TAIL
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99 108
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BY
BY
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DOMAIN 25 114
DOMAIN 115 206
DOMAIN 207 298
DOMAIN 209 332
TRANSMEM 309 332
DOMAIN 333 362
CARBOHYD 110 110
DISULFID 257 188
SEQUENCE 362 AA; 40498 36 404916 404916 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 404016 40401
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IN 207 5

TW 297 5

TEM 309 35

10 309 35

10 10 10

125 188

227 283

362 AA, 40328

1' (seq1.key)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B31_HUMAN
P30475;
                                     DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                     DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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DISULFID
SEQUENCE
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DOMAIN
DOMAIN
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I match found in sequence:

1B32_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3902 ALPHA CHAIN

(from "Swiss-prot 34")

1D 1B32_HUMAN

AC P30476;

DT 01-APR-1993 (REL. 25, CREATED)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 33, LAST ANNOTATION UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3902 ALPHA CHAIN

DE PRECURSOR (B39.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-39 B*3902.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95242308.

MEDLINE; 95242308.

MEDLINE; 95242308.

TYAN D.B.; PARHAM P.;

TISSUE ANTIGENS 45:18-26(1995).

-!-FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO TRROUGH SYSTEM.

-!-SUBUNIT: DIMEN BY STEM.

MICROGLOBULIN).

EMBL; M94053; G184166; -.

EMBL; M04243; 6458660; -.

HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA, TETRAPODA, MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 93131294.
KATO N., KARARI S., KASHIWASE K., MUELLER C., AKAZA T., JUJI
KANO K., TAKIGUCHI M.;
IMMUNOGENETICS 37:212-216(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;, DOE420Al CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E 362 AA; 4032;
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC I; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 142830;
PROSITE; PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGNAL
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qisktntqtdreslrnlrgyynqseagsht 99 108

qicktntqtdreslrnlrgyynqseagsht 99 108

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1 match found in sequence:
1B36_HDWAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN
(from "Swiss-Prot 34")
1D 1B36_HDWAN STANDARD; PRT; 362 AA.
AC P30478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qisktntqtyreslrnlrgyynqseagshi
108
 CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                         using
 FT CZ
FT D:
FT D:
SQ SI
                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                    1 match found in sequence:
1B34_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-40 B*4002.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

DOMENA J.D., JOHNSTON-DOW L., PARHAM P.;

TISSUE ANTIGENS 40:224-256(1992).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
PRECURSOR.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM.
-!- SUBGNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; L09736; G187679; -.
HSSP; P03989; 1HSA.
                                                                                                                                                                          EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                31205 MW; BFE44EFF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM: 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
24
                                                                                                                                                                                                                                                                                                           qisktntqtyreslrnlrgyynqseagsht
                                                                                                                                                  PROSITE; PS00290; IG_MHC MHC I; GLYCOPROTEIN.
                                                                                                                                                                                  181
>270
86
163
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                                                                                                                                                                                                                                                270 AA;
                                                                                                                                                                                                                                                          seq1,
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Q04826;
                                                                                                                                                              MHC I; GL
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
DISULFID
                                        SEQUENCE.
                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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DOMAIN
TRANSMEM
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65
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1 match found in sequence:
2 march 34 march 34 march 37 march 36 march 34 march 36 m
    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; C2A00916 CRC32;
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99
HYD 110 110 BY
FID 125 188 BY
227 283 BY
NCE 362 AA, 40505 MW; (99 'seq1' (seq1.key)
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DR NE PET TO DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 match found in sequence:
1B38_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
(from "Swiss-Prot 34")

ID 1B38_HUMAN STANDARD; PRT; 362 AA.
AC P30479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-40 B*4004.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
J. IMMUNDL. 142.3937-3950(1989).
I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MCROGLOBULIN).
EMBL; M24035; 6386903; --
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                 BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
NATURE 357:326-329(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
EMBL; M84383; G187716; -.
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
PRECURSOR.
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN
PRECURSOR (B40-G2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
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Y SIMILARITY.

Y SIMILARITY.

3797AB68 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qisktntqtyreslrnlrgyynqseagsht
99
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BY
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IN 115
IN 207
N 299 33
*** 333 36.
110 110
125 188
227 283
362 AA; 40430
1' (seq1.key)
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                                                                                                                                                                                                                                                                                                                                                                         EMBL, M84383; G187716; -
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE;
                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 92269955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using 'seq1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC I;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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1 match found in sequence:
1839_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
(from "Swiss-Prot 34")
1D 1839_HUMAN STANDARD; PRT; 362 AA.
AC P30480;
                                                                    HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-41 B*4101.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-42 B*4201.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
J. IMMUNOL. 142:3937-3950(1989).

J. IMMUNOL. 142:3937-3950(1989).

I. EUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.

J. SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; MA24034; G386904; -.

HSSP; P03989; 1185A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                    CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; A292D60A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 795A36FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN; SIGNAL.
                                       GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                               qisktntqtyreslrnlrgyynqseagsht
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                                                                                                                                                                                                                                                         ID 227 283
CE 362 AA; 40539
'seq1' (seq1.key)
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'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00290; IG_MHC
MIM; 142830; -.
PROSITE; PS00290; IG_MH MHC I; TRANSMEMBRANE; GSIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC I; TRANSMEMBRANE; SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 89235215.
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110
125
227
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PROSITE; PS0
                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
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TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
d using 's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                 using
                                                                                                                DOMAIN
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                                                                              CHAIN
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83

P30483

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l match found in sequence:
1B46_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
(from "Sxiss-Prot 34")
ID 1B46_HUMAN STANDARD; PRT; 362 AA.
AC P30466; .... ACCAPATION AND ARCAPATION ACCAPATION ACCAPATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBLLITY ANTIGEN, ALPHA CHAIN BW 46 B*4601.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-48 B*4801.
EXTRACELLULAR ALPHA-1.
                                                                                           SEQUENCE FROM N.A.
MEDLINE; 89235215.
MEDLINE; 89235215.
J. IMMUNGL. 142:3937-3950 (1989).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; MAGA031, 63370227; -.
HSSP; P03989; 1HSA.
MIN: 142830; -.
PROSITE; PS00290; IG_MHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; EC587DD3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qkykrqaqtdrvslrnlrgyynqseagsht
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115 206

207 298

30 333

MEM 310 333

W 314 362

W 110 110

110 110

125 188

71D 227 AA; 40440

3 'seq1' (seq1.key)
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PROSITE; PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E; PSUUZZU, --- TRANSMEMBRANE; GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
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DOMAIN
DOMAIN
TRANSMEM
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CARBOHYD
DISULFID
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SIGNAL
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SIGNAL
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          HAT THE PROCESS OF TH
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1B44 HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
(from "Swiss-Prot 34")

ID 1B44 HUMAN : STANDARD;

PRT; 362 AA.

AC P30484;

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DF HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
                                                                                                                                                                                    1 match found in sequence:
1843_HUMAN ; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA
(from "Swiss-Prot 34")
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-45(B-12) B*4501.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93056508.

MEDLINE; 93056508.

MARRIGLA J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,

MARRIGLE A.-M., ZEMMOUR J., ENIS P.D., WARD F.E., PETŽL-ERLER M.L.,

MARTELL R.W., DU TOIT E.D., PARHAM P.;

J. IMMUNOL. 149:3411-3415(1992).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, 98945539 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X61710; G32183; -
PIR; S16772; S16772.
HSSP, P03989; HRSA.
MIM; 142830; -
PROSTE; PS00290; IG_MHC.
MHC I; TRANSMERRAE; GLYCOPROTEIN; SIGNAL.
qiykaqaqtdreslrnlrgyynqseagsht
99
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N 207 298
N 299 309
N 299 309
N 299 309
N 299 309
N 310 333
N 310 310 110
FID 125 188
FID 227 A8, 40414
G'seql' (seql.key)
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DOMAIN TRANSMEM DOMAIN CARBOHYD DISULFID DISULFID SEQUENCE

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PRECURSOR.

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108
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CARBOHYD
DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                         PACE OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                      1 match found in sequence:
1B47_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA C
(from "Swiss-Prot 34")
1D 1B47_HUMAN STANDARD; PRT; 362 AA.
AC P30487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93056529.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P.;
J. IMMUNOL. 149:3563-3568(1992).
I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; MA4037; G407191; --
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-49(B-21) B*4901.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                      CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE: 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
J. IMMUNOL. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
                                                                                             Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

OBID8291 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E996F82F CRC32;
                                                                            CYTOPLASMIC TAIL.
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TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
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                                                                                                                                                                         using 'seq1' (seq1.key)
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                                                                                                                                                         AA;
115
207
209
310
334
110
125
227
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DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
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MIM; 1428
PROSITE;
MHC I; TR.
SIGNAL
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DOMAIN
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DISULFID
SEQUENCE
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qisktntqtyrenlrialryynqseagsht

83

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match found in sequence:
1B49_HUMAN:; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CH
(from "swiss-Prot 34")

ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
match found in sequence:
1B48_HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA
(from "Swiss-Prot 34")

ID 1B48_HUMAN STANDARD; PRT; 362 AA.

AC P30488;
                                                                                            01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HIGH CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW +50(B-11) B*5001.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 93056508.
MITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.;
J. IMMUNOL. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 6C8B4A34 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qisktntqtyreslrnlrgyynqseagsht
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Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X61706; G32185, -. PIR; S16773; S16773. HSSP, P03989; IHSA. MIM; 142830; -. PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FID 125 188
FID 227 283
WCE 362 AA; 40541
9 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLAB.
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EMBL; M22799; G553538; ALT_SEO.
EMBL; M22793; G553538; JOINED.
EMBL; M22794; G553538; JOINED.
EMBL; M22795; G553538; JOINED.
EMBL; M22796; G553538; JOINED.
EMBL; M22797; G553538; JOINED.
EMBL; M22797; G553538; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M22797; G55353
EMBL; M22798; G55353
PIR; B30345; B30345.
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
DISULFID
DISULFID
SEQUENCE
   83
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1B52_HDAAN; HAA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CH
   (from "Swiss-Prot 34")
1D 1B52_HDMAN STANDARD; PRT; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-51(B-5) B*5101.
EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                       MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                              POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
IMMUNGERETICS 29:297-307(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBDNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                 MEDLINE: 90207291.
ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4D846F30 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                qifktntqtyrenlrialryynqseagsht
99
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DOMAIN 115 206 EXT
DOMAIN 297 298 EXT
DOMAIN 299 332 CVT
TRANSMEM 309 332 COMAIN
CARBOHYD 110 110 BY
DISULFID 125 188 BY
SEQUENCE 327 283 BY
SEQUENCE 327 283 BY
d using 'seql' (seql.key)
                                                                                                                                                                                           J. IMMUNOL. 142:306-311(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLAB.
HOMO SAPIENS (HUMAN)
 EUTHERIA; PRIMATES
                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 89233295.
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
SEQUENCE
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1 match found in sequence:
1B53_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA C
(from "Swiss-Prot 34")
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-51(B-5) B*5104.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                      MEDLINE; 92269955.

MEDLINE; 92269955.

MEDLINE; 92269955.

MEDLICH M.P., MARRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,

MILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;

L. LUZICH M.P., THE INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.

THE INMUNE SYSTEM.

C. -1 SUBUNIT: DIRER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; 21543, GA8235, -.

R. MICROGLOBULIN).

R. MIL, 142830; -.

R. MIM; 142830; -.

R. MIN; 12880280; IG_MHC.

MICROGLOBULIN SIGNAL.

R. SIGNAL.

Z. SIGNAL.

Z. CHAIN Z. CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K., TAKIGUCHI M.;
J. IMMUNOL. 142:306-311(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-i- SUBBURN DE PAPHA CHAIN AND A BETA CHAIN (BETA-2-MINDOCTORITY).
                                                                                                                                                                                                                              ဝူ
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY. F22F08AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qifktntqtyrenlrialryynqseagshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 362 AA; 4050 using 'seq1' (seq1.key)
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sed1,
                                                                                             1B55_HUMAN
P30492;
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DOMAIN
TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                            using
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                                                                                                                                                                                                                                                                                       CHAIN
                                                                                              GEEFFE
                                                                                                                                                                                                            match found in sequence:
1B54_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
(from "Swiss-Prot 34")

ID 1B54_HUMAN STANDARD; PRT; 362 AA.

AC P30491;
                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-52(B-5) B*5201.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-53 B*5301.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                             P.
                                                                                                                                                                                                                                                01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
', 38436FE8 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                             GLYCOPROTEIN; SIGNAL
                                                                                                                                                                  qisktntqtyrenlrialryynqseagsht
99 108
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                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: DIMER OF ALPHA
MICROGLOBULIN)
EMBL, MS635; G187757; -.
PIR, A45834; A45834.
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                        MIM, 142830; THSA.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMENBRANE; GLYC
SIGNAL
                                                                                                                          Seq1.key)
     HSSP, P03989, 1HSA.
MIM; 142830; --
PROSITE; PS00290; IG_MHC.
                                                                       298
332
332
362
110
188
                           MHC I; TRANSMEMBRANE; SIGNAL 1 2
PIR; B30548; B30548
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 91033941.
                                                                                                                         62
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                                                                             DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                  DOMAIN
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DOMAIN
DOMAIN
                                                         DOMAIN
                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
83
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1 match found in sequence:
1B55_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54(BW-22) B*5401 ALPHA
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 match found in sequence:
1B56_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55(BW-22) B*5501 ALPHA
(from "Swiss-Prot 34")

ID 1B56_HUMAN STANDARD; PRT; 362 AA.

AC P30493;

DT 01-APR-1993 (REL. 25, CREATED)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55(BW-22) B*5501 ALPHA

CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-54(BW-22) B*5401.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92148136.
HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
J. IMMUNOL. 148:1155-1162(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBURIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-SUBURIN).
EMBL; M77774; G184117; -.
MICROGLOBULIN).
EMBL; M77774; G184117; -.
MIM: 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
101-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54(BW-22) B*5401 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A34A10EC CRC32;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                              362 AA
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qifktntqtyrenlrialryyngseagshi
99
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99
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L' (seq1.key)
                                                                                                                                                                                                                                                                                              STANDARD;
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1 match found in sequence:
    207
209
209
3309
110
125
362 AA;
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FT DOMAIN 20
FT DOMAIN 20
FT DOMAIN 33
FT TEANSMEM 33
FT CARBOHYD 11
FT DISULFID 12
FT DISULFID 22
SQ SEQUENCE 362
FOUND USING SEQUENCE 362
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P30495;
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TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSTATE THE THE THE TENT OF THE STATE OF THE TENT OF TH
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1B57_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55(BW-22) B*5502 ALPHA
(from "Swiss-Prot 34")

ID 1B57_HUMAN STANDARD; PRT; 362 AA.
AC P30494;
                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-55(BW-22) B*5501.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-55(BW-22) B*5502. EXTRACELLULAR ALPHA-1.
                                                                         MEDLINE; 92148136.
MEDLINE; 92148136.
MEDLINE; 92148136.
MILLOBBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
J. IMMUNOL. 148:1155-1162(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; M77778; 0184119; -.
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE; 92148136.
MEDILINE; 92148136.
J. LITTLE A.-M., PARHAM P.;
J. IMMUNOL. 148:1155-1162(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55(BW-22) B*5502 ALPHA
  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 61A75273 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qiykaqaqtdreslrnlrgyynqseagsht
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M
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DOMAIN 115 206
DOMAIN 207 298
DOMAIN 299 308
TRANSMEM 309 332
DOMAIN 333 362
CARBOHYD 110 110
DISULFID 125 188
DISULFID 125 188
SEQUENCE 362 AA; 40496 MW
rd using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M7777; G184121; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00290; IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                      MIM; 142830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                              SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
    83
```

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1 match found in sequence:
1B58_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5601 ALPHA
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-56(BW-22) B*5601.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 92148136.
HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
J. IMMUNOL. 148:1155-1162(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
1-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANORATION UPDATE)
HLA CLASS I HISTOCOMPATIBILLITY ANTIGEN, BW-56(BW-22) B*5601 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                         CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; D5BF98F0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; C91D06CC CRC32;
                                                                                    CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |-----|
qiykaqaqtdreslrnlrgyynqseagsht
99
                                                                                                                                                                                                                                                                                                       qiykaqaqtdreslrnlrgyynqseagsht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Μ¥,
                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M77776; G184123; -.. HSSP; P03989; 1HSA.
MIM; 142830; -.. PPROSITE; PSO0290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40478
                                                                                                                                                                      62 AA; 40466
' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (seq1.key)
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25
                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                              using
                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                  CHAIN
  89
1B59_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                        B-57(B-17) B*5701 ALPHA
                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW -56(BW-22) B*5602.

EXTRACELULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.
                                                                                                                       01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
101-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                              1 match found in sequence:
1B60_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990)
                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                              Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

64608CFE CRC32;
                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        362 AA
                                                                                                                                                                                                    GLYCOPROTEIN; SIGNAL.
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                 qiykaqaqtdreslrnlrgyynqseagsht
99 108
                                                                                                                                                                                                                                                                               BY
                                                                                                                                                                                                                                                                                                       MM;
                                                                                                                                                                                                                                                                                                     40460
                                                                                                                                                                   M77775; G184125; -.
                                                                                                                                                                                           PS00290; IG_MHC
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                             (seql.key)
                                                                                                                                                                                                    TRANSMEMBRANE;
                                                                                                                                                                                                                                 25
115
207
209
339
333
110
125
227
362 AA;
        m "Swiss-Prot 34")
1B59_HUMAN STA
P30496;
                                                                                                         SEQUENCE FROM N.A. MEDLINE; 92148136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 90207291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 91067476.
                                                                                                                                                                                                                                                                                                              nsing 'seql'
                                                                                                                                                                                                                                                                                                                                                                                                                     1B60_HUMAN
                                                                                                                                                                     EMBL; M77
HSSP; P03
MIM; 1428
PROSITE;
                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                    MHC I;
SIGNAL
CHAIN
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             P18465;
                                                                                                                                                                                                                                  DOMAIN
         from
                                                                                                                                                                                                                                                                                                              Found
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1 match found in sequence:
1B61_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA C
(from "Swiss-Prot 34")
1D 1B61_HUMAN
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-57(B-17) B*5701.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-57(B-17) B*5702.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MADLINE, 93055030
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
J. INMINOL. 149:3411-3415(195).
-i. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
NUCLEIC ACIDS RES. 18:6702-6702(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                      -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; M32318; G307222; -.

EMBL; X55711; G32181; -.

PIR; S12622; S12622.

PIR; S12629; D35997.

HSSP: PO3989; LHSA.

MIM; 142830; -.

PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; X61707; G32187; -.
PIR; S16774; S16774.
MIM; 142830; -.
PROSITE; PS00299; IG,MHC.
MMC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; D91DF8DD CRC32;
                                                                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rnmkasaqtyrenlrialryynqseagshi
10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                      MHC I; TRANSMEMBRANE;
```

362 AA

PRT;

STANDARD;

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1 match found in sequence:
1COl_MUNAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0101 ALPHA CHAIN
1(from "Swiss-Prot 34")
1D 1COl_HUMAN STANDARD; PRT; 366 AA.
AC P30499;
DT 01-APR-1993 (REL 25, CREATED)
DT 01-APR-1993 (REL 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL 25, LAST ANNOTATION UPDATE)
DT HA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0101 ALPHA CHAIN
GN HLAC.
    found in sequence:
MAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-78 B*7801 ALPHA CHAIN
                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HLA CLEASS I HISTOCOMPATIBILITY ANTIGEN, BW-78 B*7801 ALPHA CHAIN
PRECURSOR.
                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                         (from "Swiss-Prot 34")
D 1B63_HUMAN STA
                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MFDLINE; 93056508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using
     match foun
1B63_HUMAN
                                    match found in sequence:
1862_HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN BW-58(B-17) B*5801.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 8600824.
WAYS J.P., COPPIN H.L., PARHAM P.;
J. BIOL. CHEM. 260:11924-11933(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                           01-MAR.1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
 EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 628C2156 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 3E5E7534 CRC32;
                                                                                                                                                                                                                                                        362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
SIGNAL 124
                                                                                                                                                   rnmkasaqtyrenlrialryynqseagshi
99
                                                                                         ¥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M11799; G386885; -.
PIR; A23895; HLHUB8.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
                                                                                        EQUENCE 362 AA; 40342 using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40337
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (seq1.key)
  206
2298
332
362
1110
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA;
                                          333
110
125
227
362 7
  1115
207
299
309
                                                                                                                                                                                                                                                      1B62_HUMAN
P10319;
                      DOMAIN
TRANSMEM
                                            DOMAIN
CARBOHYD
                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
CARBOHYD
DISULFID
DISULFID
                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
FT
FT
FT
FT
FT
FT
SO
SO
SO
SO
                                                                                                                                                                                                                                                       83
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RX MEDLINE; 90217537.

RX MEDLINE; 90217537.

RA YAMAMOTO J., KANO K., TAKIGUCHI M.;

BLIMUNOL. 144:3228-3233(1990).

CC -1- FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO CC -1- FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2- MICROGLOBULIN).

CC MICROSTINS; 512191; -.

DR EMBL; X61708; G12191; -.

DR EMBL; X16775; S16775.

DR EMBL; S16775; S16775.

DR PROSITE; PS00290; IG_MHC.

WHC I; TRANSMEMBRANE; GLXCOPROTEIN; SIGNAL.

FT SIGNAL

SIGNAL

1 24 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN ALPHA CHAIN BW-78 B+7801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BM-78 B*7801.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
MEDLINE; 93056508.
MADRICAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
MITILE A.-M., ZEMMOUR J., ENIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOUT E.D., PARHAM P.;
J. IMMUNOL. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4023A9F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qifktntqtdreslrnlrgyynqseagsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MΨ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TE 362 AA; 40478
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
1115
207
209
309
333
1110
125
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
```

7,

|-----| rnmkasaqtyrenlrialryyngseagshi 99 108

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1 match found in sequence:
1C05_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 142840;
PROSITE; PSC
                                                                                                                                                                                                                                                                                                                                                                                           1C02_HUMAN
P30500;
                      DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                SEQUENCE
    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC I;
                                                                                                                     using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
  FT D
FT D
FT D
FT C
SQ SQ
                                                                                                                                                                                                                                                                                                                                                                                               HID DE SON SERVICE SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 match found in sequence:
1CO1_PANTR ; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

CALPHA CHASI I HISTOCOMPATIBILITY ANTIGEN,
CALPHA CHAIN.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN CW-1 CW*0101.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                          MEDLINE; 89215297.

ELLIS S.A., STRACHAN T., PALMER M.S., MCMICHAEL A.J.;

ELLIS S.A., STRACHAN T., PALMER M.S., MCMICHAEL A.J.;

ELLIS S.A., STRACHAN T., PALMER M.S., MCMICHAEL A.J.;

-! IMMOUL 142:3281-3285(1989).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMOUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

EMBL; MZ6429; G337239; --

HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 92391104.
MEDLINE; 92391104.
YAMASHITA S., ABE K., SHIKATA T.;
VIROLOGY 190:856-860(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
CHLA CLASZ I HISTOCOMPATIBLITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
PAN TROGLODYTES (CHIMPANZEE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE IMMUNE SYSTEM.
-!- SUBGNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL: D11383; E55339; ALT_INIT.
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
922CF5E4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 AA
                                                                                                                                                                                                                                                                                                                GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qkynrqaqtdrvslrnlrgyynqseagsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 366 AA; 40964 using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                      MIM; 142840; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLNSIGNAL
1 24
CHAIN 25 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1114
206
298
308
                                                                            SEQUENCE FROM N.A.
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309
334
125
110
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P30686;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                         CHAIN
  83
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match found in sequence:
1002_HUMAN ; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN CW-1 CW*0102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 93031775.
ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
WILLIAMS R.C., PARHAM P.;
TISSUE ANTIGENS 39:249-257(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
PRECURSOR (CW1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL, M84171, G187863; -.
HSSP, P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 98538EE9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                      CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A19B2984 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                          qkykrqaqadrvslrnlrgyynqsedgsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qkykrqaqtdrvslrnlrgyynqseagsht
99 108
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309
TID 125 15
TD 227 285
110 110
366 AA; 40842
1' (seq1.key)
                                                                                                                    40842
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TRANSMEMBRANE; GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SARBOHYD 110 110 SEQUENCE 366 AA; 4095 using 'seq1' (seq1.key)
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1 match found in sequence:
1C06_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
1C06_HUMAN STANDAED;
AC P30503;
BT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
DE PRECURSOR (CW3.2).
                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN CW-3 CW+0301.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                        SUDDIER R., DAMOTTE M., DELOVITCH T.L., TRUCY J., JORDAN B.R.,
STRACHAN T.;
MIRROGLOBULIN).
EMBL; X00495; G642239; -.
HSR, A02190; HLHUW3.
HSR, A02190; HLHUW3.
HSR, PROSSTE;
STRACHAN T. STRACHAN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G., WILLIAMS R.C., PARHAM P.; TISSUE ANTIGENS 39:249-257(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
           P04222;
20-MAR-1987 (REL. 04, CREATED)
20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
PRECURSOR (CW3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                      HONO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR ALPHA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
53795742 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL
 366 AA
                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN; SIGNAL.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qkykpqaqtdrvslrnlrgyynqseagshi
99 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 366 AA; 40744 using 'seq1' (seq1.key)
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                MHC I; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 93031775.
                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 84207947.
1C05_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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1 match found in sequence: IC12_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN (from "Swiss-Prot 34")
ID IC12_HUMAN STANDARD; PRT; 366 AA.
AC P30505;
                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN CW-3 CW*0302.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93031775.

A MEDLINE; 93031775.

A MEDLINE; 93031775.

A TISSUE ANTIGENS J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G., WILLIAMS R.C., PARHAM P.;

L TISSUE ANTIGENS 39:249-257(1992).

- I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.

- I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

R MICROGLOBULIN).

R HSSP; P03989; 1HSA.

R MIM; 142840; -.

R PROSITE; PS00290; IG_MHC.
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
PRECURSOR (CW8.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
 -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA CHAIN CW-8 CW*0801.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; ClB041C6 CRC32;
                                                                                                                                                                        CYTOPLASMIC TAIL.
         GLYCOPROTEIN; SIGNAL.
                                                                                                        25 114
115 206 EAL.
207 298 EXT.
299 308 COF
309 333
D 125 188 F
ID 227 283
IYD 110
NCE 366 AA, 40784 MW
19 'seql' (seql.key)
                                                                                                                                                                                                                                                                                   qkykrqaqtdrvslrnlrgyynqseagshi
99 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E; PSUUZ>V,
TRANSMEMBRANE; GI
                                                                                                                         DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC I;
SIGNAL
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                                                                                                              DOMAIN
                                                                                                                                                                                                                                using
                                                                                         CHAIN
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CYTOPLASMIC TAIL. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.

334 125 227 110 366 AA;

DOMAIN DOMAIN TRANSMEM DOMAIN DISULFID DISULFID CARBOHYD SEQUENCE

A59EF965 CRC32;

40772 MW;

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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                             SEQUENCE FROM N.A.
MEDLINE; 92269955.
  PRECURSOR.
                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                 using
 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 match found in sequence:
1C14_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0803 ALPHA CHAIN
(from 'Swiss-Prot 34")
1D 1C14_HUMAN STANDARD; PRT; 366 AA.
AC P30507;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DF 101-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DF HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0803 ALPHA CHAIN
                                                                                                               match found in sequence:
1C13_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0802 ALPHA CHAIN
(from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN CW-8 CW*0802.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                    MEDILINE; 93031775.

X MEDILINE; 93031775.

A WILLIAMS R.C., PARHAM P.;

I ISSUE ANTIGENS 39:249-257(1992).

- I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INAUNE SYSTEM.

C -1- SUBGINIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROLODININ).

REMBL; M84173; G187867; -.

R HSSP; P03989; HSSA.

MIM: 142840; -.

R PRISSIF PS00290; IG_MHC.

R PROSITE; PS00290; IG_MHC.

TITALIAMSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                           5
P
                                                                                                                                                                 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBLITY ANTICEN, CW-8 CW*0802 ALPHA CHAIN
                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 450BD038 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC TAIL.
                                                                                                                                                PRT;
                                                   qkykrqaqtdrvslrnlrgyynqseagsht
99 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qkykrqaqtdrvslrnlrgyynqseagsht
99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 366 AA; 40871 using 'seq1' (seq1.key)
                                                                                                                                                STANDARD;
Found using 'seql' (seql.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
115
207
209
334
125
227
110
                                                                                                                                                                                                            PRECURSOR (CW8.2).
                                                                                                                                              1C13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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1 match found in sequence:
1C15_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1201 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")
ID 1C15_HUMAN STANDARD; PRT; 366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P30508;
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOFATION UPDATE)
HIA CLASS I HISTOCOMPATIBILLITY ANTIGEN, CW*1201 ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN CW-8 CW*0803.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
WALLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
WALLIAMS S.7.326-329(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBGUITY: DIRER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; 215144; G28357; --
MICROGLOBULIN).
MMIX; PA2040; --
PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKATA H., SONODA A., BECK S., HEYES J.M., BODMER J.G., INOKO H.; SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBMIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MCROGLOBLIN).
EMBL, M21963; G188541; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKATA H., INOKO H., ANDO A., HARANAKA M., WATANABE B., TSUJI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
'; F54756A6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                           PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qkykrqaqtdrvslrnlrgyynqseagsht
99 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E 366 AA; 4087
'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 88330144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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HA11_MOUSE
P01899;
                                                                                                       CXX_HUMAN
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H2-D.
                                                                                                        83
                                                                                                                                                                                                                                                                    1 match found in sequence:
1017_HUMAN; HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")
1D 1017_HUMAN STANDARD; PRT; 366 AA.
AC P30510;
                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECURSOR (HLA-CB-1).
                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN CW*1201.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN CW*1401.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. IMMUNOL. 143:1372-1378(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUILT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; M28171; G386905; -.
HSSP; P03899; 14SA.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 89309827.
TAKIGUCHI M., NISHIMURA I., HAYASHI H., KARAKI S., KARIYONE A.
                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 0E9BB9A5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 05F828B2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC 1; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL. SIGNAL
                           GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                              qkykrqaqadrvslrnlrgyynqseagsht
                                                                                                                                                                                                                                                                                              W.
                                                                                                                                                     EQUENCE 366 AA; 40851 using 'seq1' (seq1.key)
HSSP; P03989; 1HSA.
MIM; 142840; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYC
SIGNAL 1
                                                                          DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
DISULFID
                                                                                                                                  DISULFID
                                                                                                                                                     SEQUENCE
                                                                 DOMAIN
                                               CHAIN
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D-B ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                       21-JUL 1986 (REL. 01, CREATED)
1-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANOUATION UPDATE)
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN PRECURSOR.
                                                                                      1 match found in sequence:
1CXX_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN.
(from "SWISS-Prot 34")
                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-ARR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILLITY ANTIGEN, C-4 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 match found in sequence:
HA11_MOUSE ; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
  (from "Swiss-Prot 34")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
i; CD5F7D52 CRC32;
                                                                                                                                      342 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qkykrqaqadrvslrnlrgyynqsedgsht
75
qkykrqaqtdrvslrnlrgyynqseagsht
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38082 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M1886; G386777; -PIR, A4512; HLHUG4. HSSP, P03989; 1HSA. MIM; 142840; -PROSITE; PS00290; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 342 AA; 3808 using 'seql' (seql.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
274
284
342
386
386
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DOMAIN 25 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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MEDLINE; 88060499.
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Fri May 23 08:52:43 1997

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**X FAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 25-296.

**X FAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 25-296.

**A YOUNG A.C. M., ZHANG W., SACCHETTINI J.C., NATHENSON S.G.;

**CELL 76:39-50(1994).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- FUNDINIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

**EMBL; M18523; G387452; -...

**EMBL; M18523; G397452; -...

**EMBL; M10129; G199341; ALT_INIT.**

**PRESENTE; PSO(129; G19341; ALT_INIT.*

**PRESENTE; PSO(129; G1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN.
EXTRACELLOLAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J., GOODENOW R.S.;
J. IMMUNOL. 139:3878-3885(1987).
                                                                                                 STRAIN-NOD/LT;
GIRGIS K.R., CAPRA D.J., STROYNOWSKI I.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                    SEQUENCE OF 25-122.
MEDLINE; 81142266.
MALOY W.L., NATHENSON S.G., COLIGAN J.E.;
J. BIOL. CHEM. 256:2863-2872(1981).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                               SEQUENCE OF 105-362 FROM N.A.
MEDLINE, 83005712.
REYES A.A., SCHOLD M., WALLACE R.B.;
IMMUNGENETICS 16:1-9(1982).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 253-308 AND 332-358
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 83005713.
MALOY W.L., COLIGAN J.E.;
IMMUNOGENETICS 16:11-22(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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DOMAIN
TRANSKEM
DOMAIN
DISULFID
DISULFID
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HELIX
TURN
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1 match found in sequence:
HA14 MOUSE; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID HA14 MOUSE
AC P14427;
AC P14427;
DT 01-JAN-1990 (REL, 13, CREATED)
DT 01-JAN-1990 (REL, 13, LAST SEQUENCE UPDATE)
DT 01-TAN-1990 (REL, 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL, 33, LAST ANNOTATION UPDATE)
DT 01-FEB-1996 (REL, 33, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE; 86169714.

X MEDILINE; 86169714.

A SCHEPART B.S., TAKAHASHI H., COZAD K.M., MURRAY R., OZATO K.,
A PPELLA E., FREILINGER J.A.;
J. IMMUNOL. 136:3489-3495(1986).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-REAL) MIZOROLOBOULIN).

R EMBL; MIZOROLOBOLIN).
R RSSP; P01901; 1VAA.
R RSSS; P01901; 1VAA.
R PROSETTE; PS00290; IG_MMC.
MMC I; TRANSMEBRANE; GLEVCOPROTEIN; SIGNAL.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY STHILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6C5B86B5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |-----|
| qkakgqeqwfrvslrnllgyynqsaggsht
| 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40836 MW;
FT HELLX 176 185
FT TURN 186 186
FT TURN 197 196
FT TURN 200 204
FT STRAND 210 210
FT STRAND 220 221
FT STRAND 220 221
FT STRAND 226 232
FT STRAND 226 232
FT STRAND 225 232
FT STRAND 225 232
FT STRAND 225 232
FT STRAND 225 243
FT STRAND 246 247
FT STRAND 246 247
FT STRAND 246 247
FT STRAND 256 251
FT TURN 256 271
FT TURN 256 271
FT TURN 278
FT STRAND 278
FT TURN 278
FT STRAND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
368
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TRANSMEM
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DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
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DOMAIN
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1 match found in sequence:
HLAH_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR (from "Swiss-Prot 34")
ID HLAH_HUMAN STANDARD; PRT; 362 AA.
AC POl893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALLSEEN M., MALISSEN B., JORDAN B.R.;

MALLSEEN M., MALLSSEN B., JORDAN B.R.;

PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).

1 FROCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

1-- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

REMBL; VO0526: G386873; ALT_INIT.

R PIR; A02189; HLHU12.

R PROSITE; PS00290; IG_MHC.

R PROSITE; PS00290; IG_MHC.

R PROSITE; PS00290; IG_MHC.

R MACI I; TRANSMERRANE; GLYCOPROTEIN; SIGNAL.

I SIGNAL

CHAIN

25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
(HLA-AR) (HLA-12.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLAH.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total Elapsed 00:04:09.00
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BY SIMILARITY.
BY SIMILARITY.
7; 5E610F63 CRC32;
SQ SEQUENCE 368 AA; 41342 MW; 7D4C13C1 CRC32; Found using 'seq1' (seq1.key)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- Search Statistics
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96 105
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99 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPU
00:03:44.14
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Number of sequence hits:
Number of separate matches:
Number of sequence hits saved:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |-----|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 82151002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Thu May 22 08:45:38 1997; MasPar time 1.81 Seconds 70.334 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-7 (1-6) from US08653294.pep 49 1 YRLAIR 6

Title: Description: Perfect Score:

Sequence:

59021 seqs, 21210388 residues PAM 150 Gap 15 Searched:

Scoring table:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 22.440; Variance 22.471; scale 0.999

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* a \$
sult Query
No. Score Match Length DB

Pred. No.

Result

No matches found.

Search completed: Thu May 22 08:45:46 1997 Job time: 8 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Run on:

Thu May 22 08:50:08 1997; MasPar time 2.66 Seconds 128.376 Million cell updates/sec

Tabular output not generated.

>US-08-653-294-36 (1-12) from US08653294.pep 98 1 YRLAIRRIALRY 12 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

89912 seqs, 28507787 residues

Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 26.905; Variance 45.950; scale 0.586

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description sult Query
No. Score Match Length DB ID Result

Å

Pred. No.

No matches found.

Search completed: Thu May 22 08:50:18 1997 Job time: 10 secs.

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protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Thu May 22 08:49:45 1997; MasPar time 1.88 Seconds 135.656 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-653-294-36 (1-12) from US08653294.pep 98

Title: Description: Perfect Score: Sequence:

1 YRLAIRRIALRY 12

PAM 150 Gap 15 Scoring table:

59021 segs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Maximum DB seq length 60 Post-processing:

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 28.088; Variance 37.415; scale 0.751

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. Description ü lesult Query
No. Score Match Length DB Result

Search completed: Thu May 22 08:49:51 1997 Job time : 6 secs.

No matches found

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2.89e+00
2.89e+00
4.96e+00
ADENOSINE AZA RECEPTO
APOLIPOPROTEIN(A) (EC
MULTIDRUG RESISTANCE
1 AA2A_CANFA
1 APOA_MACMU
6 MEXA_PSEAE
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4 .96e+00 4 .96e+00 4 .96e+00 4 .96e+00 4 .96e+00 4 .96e+00 4 .96e+00 8 .43e+00 1 .42e+01 1 .42e+01 1 .42e+01 1 .42e+01 1 .42e+01 1 .42e+01 2 .36e+01	JRSOR	9		ANTIGEN,	
CYTCCHROME C OXIDASE DNA-DIRECTED RNA POLY MUTS PROTEIN HOMOLOG DNA-DIRECTED RNA POLY DNA-DIRECTED RNA POLY CAD PROTEIN (CONTAINS GENE 19.2 PROTEIN. ADENOSINE AZB RECEPTO 60 KD INNER-MEMBRANE COATOMER BETA SUBUNIT GTP-BINDING PROTEIN ATP-DEPENDENT HELICAS PROBABLE RNA-DIRECTED PROBABLE	59 AA. DATE) UPDATE) N, B-1 ALPHA CHAIN PRECURSOR TA; TETRAPODA; MAMMALIA;	I P., VAN SEVENTER G., DBJ DATA BANKS.	D A BETA CHAIN (BETA-2-	OCOMPATIBILITY HA-1. HA-3. E.	DB 1; Length 359;
COXX YEAST RPA1_SULAC MSH1_YEAST RPB1_SCHAO PYR1_HUMAN PYR1_HUMAN PYR1_MESAU PYR1_MESAU PYR1_MESAU PYR1_MESAU PYR1_MESAU PYR1_MESAU PYR1_MESAU PYR1_MESAU RPP1_COND RRPO_CNV R	T; 3 NCE UP ATION ANTIGE	N.A. 0641. ONKER M., KLEIN D., IVANYI P. 5-2774(1988). B-1989) TO EMBL/GENBANK/DDBJ I	CHAIN AN	CHLA CLASS I HIST B-1 ALPHA CHAIN. EXTRACELLULAR ALP EXTRACELLULAR ALP EXTRACELLULAR ALP CONNECTING PEPTID CYTOPLASMIC TAIL. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. W; 5395FFC9 CRC32;	Score 49;
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991.8 991.8 991.8 997.7 985.7 985.7 98.7 98.7 98.7 98.7 98.7 98.7 98.7 98	O (REL. O (REL. O (REL. 3 (REL. I HISTO DYTES (G METAZO)	FOM N.A 9030641 , JONKE] 2765-27 (FEB-198	MUNE SY T: DIME! LOBULIN 115, G75 7; S035, 7; S035, 89; 148, 89; 148, NSMEMBRA	21 21 21 203 295 396 330 121 121 223 106 359 AA	
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Local Similarity 100.0%;
nes 6; Conservative
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EMBL; X60255; G22866; -
PIR; JH0539; JH0539.
HSSP; P03989; JHSA.
PROSITE; PS00290; IG_MHC.
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206
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188
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227
110
362 AA;
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REVISIONS TO 78.
MEDLINE; 93056529.
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P30379;
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SIGNAL
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                                                                                                                     11849_HUMAN STANDARD; PRT; 362 AA.
1184644;
101.NOV-1990 (REL. 16, CREATED)
101.NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
101.FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-51(B-5) B*5101.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR ALPHA-3 CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
MEDILINE; 90207231.
ENNIS P.D., SEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
 No. 5.42e-01;
Mismatches 0;
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SY SIMILARITY.

SY SIMILARITY.

4D846F30 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M3219; G30723; -. M22792; G55353; ALT_SEQ., M22786; G55353; JOINED., M22788; G55353; JOINED., M22788; G55353; JOINED., M22789; G55353; JOINED., M22790; G55353; JOINED., M22790; G55353; JOINED., L41087; G735902; -. L41086; G735902; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
Best Local Similarity 100.0%;
Matches 6; Conservative
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PIR; A30548; A30548.
HSSP; P03989; IHSA.
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227
362 AA;
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                                            rialry 104
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MIM; 142830;
                                                                            RIALRY
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TRANSMEM
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DISULFID
SEQUENCE
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P30487;
01-APR-1993 (REL. 25, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PHIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                           01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA GORILLA GORILLA GORILLA, EUKARYOTA, METAZOA, CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A.
MEDILNE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
J. EXP. WED. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GGGO-BOIOL ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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Pred. No. 5.42e-01;
0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
J. IMMUNOL. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 2E33E2BB CRC32;
362 AA
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PRT;
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BY SIMILARITY.
F22F08AB CRC32;
    283 E
40560 MW;
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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SIGNAL 124
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309
333
125
227
362 AA;
    227
362 AA;
                                                                                                              103 rialry 108
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| RIALRY
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY. ANTIGEN, ALPHA CHAIN B-51(B-5) B*5104.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                                                                                                                                                                                      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-49(B-21) B*4901.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P.;
J. IMMUNOL. 149:3563-3568(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBGUIL IN JERR OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
EMBL; M24037; G407191; -.
HISSP: P03899; LHSA.
MIM: 142830; -.
MIM: 142830; -.
MIM: 142830; -.
MIM: 122830; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E996F82F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                 MM:
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Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 40581
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206
2298
3308
332
362
1110
1188
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SIGNAL 1 24
CHAIN 25 363
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115
207
310
310
110
125
227
362 AA;
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1 RIALRY
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1B52_HUMAN
P30489;
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SEQUENCE
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DOMAIN
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1B03_GCRGO STANDARD; PRT; 362 AA.

p30381.

01-APR-1993 (REL. 25, CREATED)

01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)

01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.

GORILLA GORILLA GORILLA (LOWIAND GORILLA).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11002_GORGO STANDARD; PRT; 362 AA.
11002_GORGO STANDARD; PRT; 362 AA.
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SANOTATION UPDATE)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA GORILLA CHAIN PRECURSOR.
EUKARKOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92078660.
LAMLOR D.A., WARRED E., TAYLOR P., PARHAM P.;
LAMLOR D.A., WARRED E., TAYLOR P., PARHAM P.;
J. EXP. MED. 114:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBJUTION IN THE PRESENTATION OF ERRA-2-
MICROGLOBULIN).
EMBL: X60254; G22870; -.
PRIX, J040541; HO544.
HSSP: P03999; 185A.
PROSITE; PS00290; IG.MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GGGO-BOILO3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
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Pred. No. 5.42e-01;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
', FEA6A941 CRC32;
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MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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103 rialry 108
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| RIALRY 6
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SEQUENCE
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DISULFID
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TRANSMEM
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LOPEZ DE CASTRO J.A.;
PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMOUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                               BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BO102 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECURSOR (B-27K) (B27.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 362;
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SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; L
Pred. No. 5.42e-01;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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NY SIMILARITY.

SY SIMILARITY.

3CF119AD CRC32;
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MIM: 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSHEMBRANE; GLYCOPROTEIN; SIGNAL.
SIGNAL.
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J. EXP. MED. 174:1491-1509(1991)
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EMBL, X03667, G871296, JOINED.
EMBL, L38504, G896271, -.
PIR, B25092, HLHUBK.
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Best Local Similarity 100.0%;
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362 AA;
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| RIALRY 6
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1815_HUMAN
P10317:
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CARBOHYD
SEQUENCE
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN B-27 B*2702.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
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EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                    Gaps
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HAYASHI H., OCBA T., NAKAYAMA S., SEKIMATA M., KANO K.,
HAYASHI M.;
IMMUNOGENETICS 32:195-199(1990).
-!-FUNGURE SYSTEM.
-!-FUNGUNE SYSTEM.
-!-SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MCROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                              11B54_HUMAN STANDARD; PRT; 362 AA.
P30491;
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
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Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 9798FOBB CRC32;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 2BDC746E CRC32;
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206
208
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P03989; 1HSA.
MIM; 142830; -
PROSITE; PS00290; IG_MHC
                                255
207
207
209
3309
1130
125
362
AA,
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309
110
125
227
362 AA;
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HLA CLASS I HISTOCOMPATIBLLITY ANTIGEN, ALPHA CHAIN B-57(B-17) B*5702.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLAH_HUMAN STANDARD; PRT; 362 AA.
P01893;
21-JUL-1986 (REL, 01, CREATED)
01-APR-1993 (REL, 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL, 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE; 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
MALISSEN M., MALISSEN B., JORDAN B.R.;
PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMONE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 5; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

628C2156 CRC32;
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BY SIMILARITY.
BY SIMILARITY.
; 5E610F63 CRC32;
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                                                                                                               GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, V00525; G386873; ALT_INIT.
PIR; A02189; HLHU12.
HSSP; P03989; 1HSA.
MIM; 142925; -
PROSITE; PS00299; IG_MHC.
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
EMBL; X61707; G32187; -..
PIR; S16774; S16774.
HSSP; P03989; IHSA.
MIM; 142830; -..
PROSITE; PS00290; IG_MHC.
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2208
3308
332
1110
283
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2206
3332
3332
1110
283
                                                                                                    MHC I; TRANSMEMBRANE; SIGNAL 1
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2007
2007
3009
3333
1120
1255
362 AA;
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110
227
362 AA;
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DOMAIN
TRANSMEM
DOMAIN
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DISULFID
SEQUENCE
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TRANSMEM
DOMAIN
CARBOHYD
DISULFID
SEQUENCE
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1B61_HUMAN STANDARD; PRT; 362 AA.
1B61_HOMAN STANDARD;
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW 58(B-17) B*5801.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                           X MEDLINE; 86008247.

A WAYS J.P., COPPIN H.L., PARHAM P.;

J. BIOL. CHEM. 260:11924-11933(1985).

C -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

C -!- FUNCTION: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

R MINS A23895; HIGHB8.

R HSSP; P03899; HSA.

R HSSP; P03899; ILSA.

R MIN; 142830; -.

R PROSITE; PS00299; IG_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 93056508.
MEDLINE; 93056508.
MEDLINE; 93056508.
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L., MARTELL R.W., DU TOIT E.D., PARHAM P.;
J. IMMUNOL. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
CHAIN PRECURSOR.
                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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Pred. No. 5.42e-01;
0; Mismatches 0; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 3E5E7534 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
                             362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOPROTEIN; SIGNAL.
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
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Local Similarity 100.0%;
les 6; Conservative
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                          STANDARD;
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332
362
1110
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115
207
299
309
333
110
125
362 AA;
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01-MAR-1989
                        1B62_HUMAN
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DOMAIN TRANSMEM DOMAIN CARBOHYD

DOMAIN DOMAIN DOMAIN

SIGNAL

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Query Match

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1A04_GORGO STANDARD; PRT; 365 AA.
P30378;
01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-A0501 ALPHA CHAIN PRECURSOR.
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
EUNARROTA, METAZOA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CRAIN B-$7(B-1) B*$701. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2.
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 91067476.
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
NUCLEIC ACIDS RES. 18:6702-6702(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMONE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
J. EXP. MED. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBJUNIA.
MICROGLOBULINI).
EMBL; X60256; G22860; -.
PIR; JH0537; JH0537.
HSSP; PO1892; HHG.
PROSTITE; PS002290; IG_MHC.
MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
SIGNAL
1 24
SYSTEMATTY.
25 365 CLASS I HISTOCOMPATIBILITY ANTIGEN,
  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                              SEQUENCE FROM N.A.
MEDILINE; 90207291.
ENNIS P.D. , SEMMOUR J., SALTER R.D., PARHAM P.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, D91DF8DD CRC32;
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MIM; 142830; -.
PROSITE; PS00290; IG_MHC.
MHC I; TRANSMEWBERANE; GLYCOPROTEIN; SIGNAL.
SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40224 MW;
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Local Similarity 100.0%;
les 6; Conservative
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110
125
227
362 AA;
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TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                  01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
HARA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(8-5) B*5201 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BW-52(B-5) B*5201.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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MEDLINE: 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO 1
TAKIGUCHI M.;
J. IMMUNOL. 142:306-311(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS:
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMEN OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 1; Length 362;
Pred. No. 5.42e-01;
0; Mismatches 0; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 38436FE8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22799; G553538; ALT_SEQ.
REML; M22793; G553538; ALT_SEQ.
REML; M22794; G553538; JOINED.
REMBL; M22795; G553538; JOINED.
REMBL; M22795; G553538; JOINED.
REMBL; M22796; G553538; JOINED.
REMBL; M22798; JOINED
                                                                                                                              362 AA
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                              STANDARD;
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332
332
342
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188
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HOMO SAPIENS (HUMAN).
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227
362 AA;
103 rialry 108
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| RIALRY 6
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| RIALRY
                                                                                                        LT 13
1B53_HUMAN
P30490;
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DOMAIN
DOMAIN
TRANSMEM
DOMAIN
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DOMAIN CHAIN

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Gaps

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GOGO-A0501 ALPHA CHAIN.	EXTRACELLULAR ALPHA-1.	EXTRACELLULAR ALPHA-2.	EXTRACELLULAR ALPHA-3.	CONNECTING PEPTIDE.		CYTOPLASMIC TAIL.	BY SIMILARITY.	BY SIMILARITY.	BY SIMILARITY.	40895 MW; 520225DF CRC32;	0%; Score 49; DB 1; Length 365; 0%; Pred. No. 5.42e-01; ve 0; Mismatches 0; Indels
	114	206	298	308	332	365	188	283	110	4089	100.0 100.0 vativ
	25	115	207	299	309	333	125	227	110	365 AA;	100.0%; imilarity 100.0%; 6; Conservative
	DOMAIN	DOMAIN	DOMAIN	DOMAIN	TRANSMEM	DOMAIN	DISULFID	DISULFID	CARBOHYD	SEQUENCE	ubery Match Best Local Similarity 100.0%; Matches 6; Conservative
F	FI	FJ	FT	БŢ	FI	ΕŢ	FJ	FI	F	S	Q A A

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